


```

RL Patent number JP 1997224673-A/8, 02-SEP-1997.
RL AGENCY OF IND SCIENCE & TECHNOL, HITACHI CHEM CO LTD, TAISHO PHARMACEUT
CO LTD.
CC OS None
CC OC Artificial sequences.
CC PN JP 1997224673-A/8
CC PD 02-SEP-1997
CC PF 22-FEB-1996 JP 1996034898
CC PI TAHARA KAZUMASA, NISHIKAWA SATOSHI, YAMADA AKIRA,
PI HANADA KAZUNORI
CC PC C12N15/09, A61K48/00, A61K48/00, A61K49/00, C07H21/02,
CC PC C07H21/04,
CC C12N9/16, C12Q1/68//A01N63/00;
CC CC strandedness: Single;
CC CC topology: Linear;
CC CC hypothetical: No;
CC CC key Location/Qualifiers
CC FT source 1.16
CC FT /organism="Artificial sequences"
CC FT Location/Qualifiers
CC FH key
CC FH source 1.16
CC FH /organism="unidentified"
CC FH /db_xref="taxon:32644"
CC FT
CC FT
SQ Sequence 16 BP: 2 A; 4 C; 6 G; 4 T; 0 other;

Query Match 55.6%; Score 15; DB 11; Length 16;
Best Local Similarity 73.3%; Pred. No. 4.29e+02;
Matches 11; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

D5 1 CCTCAGGCTGAGT 15
||:|||||:||||:
QY 13 CCTCAGGCTGAGT 27

RESULT 4
LOCUS 123911 20 bp DNA PAT 21-NOV-1996
DEFINITION Sequence 13 from patent US 5541060.
ACCESSION 123911
NID 91603781
VERSION 123911.1 GI:1603781
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Bell,G.I., Stoffel,M., Takeda,J., Vionnet,N., Yasuda,K.,
Plikis,S.J., Zouali,H., Velho,G., Cohen,D. and Froguel,P.
TITLE Detection of glucokinase-linked early-onset non-insulin-dependent
diabetes mellitus
JOURNAL Patent: US 5541060-A 13 30-JUL-1996;
FEATURES
source Location/Qualifiers
1.20
BASE COUNT 6 a /organism="unknown" 5 t
ORIGIN 5 c 4 g

Query Match 55.6%; Score 15; DB 25; Length 20;
Best Local Similarity 89.5%; Pred. No. 4.29e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

DB 1 TCAGATTCTGAGGCTCAAA 19
||||| |||||||
CP 25 TCAGACCTGAGGCTCAAA 7

Search completed: Mon Aug 2 11:45:05 1999
Job time : 489 secs.

```

WIRE

(7M)

Release 3.1A John F. Collins, Biocomputing Research Unit.
Copyright (c) 1993-1998 University of Edinburgh, U.K.
Distribution rights by Oxford Molecular Ltd

MPsrch_n n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Mon Aug 2 11:56:31 1999; Mspat time 25.66 Seconds
225,494 Million cell updates/sec

Tabular output not generated.

Title: >US-09-121-239-23
(1-27) from US09121239.seq
Description: Perfect Score: 27
N.A. Sequence: 1 UCUCACUUGAGCCUCAGGUCUGAGU 27
Comp: AGACTGMAACTCGAGTCCCAAGACTCA

Scoring table: TABLE default
Gap 10

Match STD : Dbase 0; Query 0

Searched: 271905 segs, 107135622 bases x 2

Pct-Processing: Minimum Match 0%

Listing first 1000 summaries
Maximum DB seq length 50

Database:

n-geneeq35
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part32 33:part33
34:part34 35:part35 36:part36 37:part37 38:part38
39:part39 40:part40 41:part41 42:part42 43:part43
44:part44 45:part45 46:part46 47:part47 48:part48
49:part49 50:part50 51:part51 52:part52 53:part53
54:part54 55:part55 56:part56 57:part57 58:part58
59:part59 60:part60

Statistics: Mean 5.548; Variance 3.416; scale 1.624

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	24	88.9	50	51	V66349	1.07e-03
2	24	88.9	50	19	T15571	1.07e-03
3	24	88.9	50	28	T42417	1.07e-03
4	24	88.9	50	15	O86626	1.07e-03
5	22	81.5	22	3	O1A244	1.41e-02
6	22	81.5	22	10	O63302	1.41e-02
7	22	81.5	22	36	T88787	1.41e-02
8	20	74.1	50	40	V01841	1.73e-01

9	19	70.4	24	50	V58784	5.32e-01
10	17	63.0	23	15	O86124	6.31e-00
11	17	63.0	27	28	T62502	5.31e+02
12	16	59.3	27	28	T62502	2.08e-01
13	15	55.6	16	35	T91968	6.45e+01
14	15	55.6	20	9	O51057	6.45e+01
15	15	55.6	20	45	V39479	6.45e+01
16	15	55.6	40	45	V39479	6.45e+01
17	15	55.6	40	45	V39479	6.45e+01
18	15	55.6	40	45	V39479	6.45e+01
19	14	51.9	29	29	O56492	1.94e+02
20	14	48.1	21	3	T38971	5.64e+02
21	13	48.1	21	2	O08506	5.64e+02
22	13	48.1	21	2	O10345	5.64e+02
23	13	48.1	21	7	O42804	5.64e+02
24	13	48.1	22	29	T63590	5.64e+02
25	13	48.1	24	46	V42514	5.64e+02
26	13	48.1	27	54	V95538	5.64e+02
27	13	48.1	29	5	O28596	5.64e+02
28	13	48.1	33	31	T77273	5.64e+02
29	13	48.1	42	36	T70502	5.64e+02
30	13	48.1	42	36	O23427	5.64e+02
31	13	48.1	42	39	V12519	5.64e+02
32	13	48.1	42	50	V38133	5.64e+02
33	13	48.1	42	28	T37221	5.64e+02
34	13	48.1	42	7	O44165	5.64e+02
35	13	48.1	45	28	T51509	5.64e+02
36	13	48.1	45	28	V30882	5.64e+02
37	12	44.4	22	52	V51543	1.57e+03
38	12	44.4	24	40	V12138	1.57e+03
39	12	44.4	27	59	V98214	1.57e+03
40	12	44.4	28	9	V98051	1.57e+03
41	12	44.4	28	9	O49288	1.57e+03
42	12	44.4	41	51	V51151	1.57e+03
43	12	44.4	43	44	V27600	1.57e+03

Note: Post-processor removed 955 summaries from list due to search parameters CMC

ALIGNMENTS

RESULT 1
ID V66349; standard; DNA: 50 BP.
AC V66349;
DT 06-JAN-1999 (first entry)
DE CML-2 chromosomal translocation t(9;22) primer.
KW CML-2 chromosomal translocation t(9;22): block splice template;
KW autocatalytic RNA amplification; primer; ss.
OS Synthetic.
PN US5824518-A.
PS 20-OCT-1998.
PF 06-JUN-1995; 469067.
PR 10-JUL-1990; US-550837.
PR 11-JUL-1989; US-379501.
PR 06-JUN-1995; US-469067.
PA (GENP-) GEN-PROBE INC.
PI Bultr 7T Kacian DL;
DR F01: 98-582557/49.
PT Block splice template useful for amplification of nucleic acids 3' of
PT comprises two nucleic acid regions, the first region located 3' of
PT the second region and blocked at its 3' terminus to inhibit primer
PT extension by a DNA polymerase
PS Example 15: Column 9; 51pp; English.
PS V66349-50 represent CML-2 chromosomal translocation t(9;22) primers,
CC for the (+) and (-) strands respectively. The primers are used to
CC exemplify the invention, together with probe V66351. The specification
CC describes methods of synthesizing multiple copies of a target nucleic
CC acid sequence autocatalytically under conditions of substantially
CC constant temperature, ionic strength and pH are provided in which
CC multiple RNA copies of the target sequence autocatalytically
CC generate additional copies. The target sequence is a block splice
CC template which comprises two nucleic acid regions. The first region is
CC located 3' of the second region and is blocked at its 3' terminus to

CC inhibit primer extension by a DNA polymerase, and the second region
CC comprises a promoter sequence recognised by an RNA polymerase. The
CC methods are used to amplify nucleic acids, especially RNA, for
CC analysis, cloning or probe production.
SQ Sequence 50 BP; 17 A; 12 C; 11 G; 10 T;

Query Match 88.9%; Score 24; DB 51; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.07e-03;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Dn 27 actcagaccctgagctcaagtc 50
Cp 27 ACTCAGACCCTGAGCTCAAGTC 4

RESULT 2
ID T15571 standard; DNA; 50 BP.
AC T15571;
DE 17-JUL-1996 (first entry)
DE CML-2 chromosomal translocation major breakpoint t(9;22) (-) primer.
KW CML-2 chromosomal translocation major breakpoint; t(9;22); primer;
KM auto-catalytic; synthesis; RNA target sequence; assay; detection;
KW quantification; ss.
OS Synthetic.
PN US5480764-A.
PD 02-JAN-1996.
PF 11-JUL-1989; 379501.
PR 11-JUL-1989; US-379501.
PR 10-JUL-1990; US-550837.
PA (GENP-) GEN-PROBE INC.
PI Fultz TJ, Kacian DL;
DE WPI; 96-068248/07.
PT Auto-catalytic synthesis of multiple copies of an RNA target
PT sequence - uses cooperative action of a DNA and RNA polymerase in
PT presence of RNase H, useful for detection of target sequence e.g. in
PT clinical or environmental sample
PS Example: Columns 9-10; Sipp; English.
CC The present sequence is a primer for the CML-2 chromosomal
CC translocation major breakpoint t(9;22), which was used to
CC demonstrate an improved method for synthesising multiple copies of
CC a RNA target sequence. The method comprises combining the target
CC with a primer which hybridises to the 3'-terminal portion of the
CC target, a promoter primer which hybridises with a portion of the
CC DNA primer extension prod., reverse transcriptase, RNase H and
CC transcriptase. It can be used as a component of an assay to detect
CC and/or quantitate specific target sequences in clinical,
CC environmental or forensic samples. It also has the advantages of
CC being autocatalytic, using the cooperative action of a DNA
CC polymerase, e.g. a reverse transcriptase and avoids repetitive
CC manipulations of reaction conditions, e.g. temp., ionic strength
CC and pH.
SQ Sequence 50 BP; 17 A; 12 C; 11 G; 10 T;

Query Match 88.9%; Score 24; DB 19; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.07e-03;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Dn 27 actcagaccctgagctcaagtc 50
Cp 27 ACTCAGACCCTGAGCTCAAGTC 4

RESULT 3
ID T42417 standard; DNA; 50 BP.
AC T42417;
DE 28-APR-1997 (first entry)
DE CML chromosomal translocation primer #1.
KW HIV probe; primer; amplify; polymerase chain reaction; microorganism;
KM BCL-2; PCR; hepatitis B virus; HBV; CML; ss.
OS Synthetic.
PN EP-731175-A2.
PD 11-SEP-1996.
PF 10-JUL-1990; 307503.

PR 11-JUL-1989; US-379501.
PA (GENP-) GEN-PROBE INC.
PI McDonough S;
DR WPI; 96-403995/41.
PT Detection of HIV nucleic acids in samples - using new specific
PT oligo-nucleotide(s) for the amplification and detection of target
PT sequences.
PS Disclosure; Page 8; 66pp; English.
DE T42417-T42419 represent primers and a probe for the CML chromosomal
CC translocation t(3;22). These sequences can be used in modified
CC of the kits of the invention. The kits of the invention, are for
CC detecting the presence of HIV nucleic acid sequences in a sample.
CC kits comprise two amplification primers (such as T40182 and T40183),
CC a probe (such as T42404) for detection of the amplified sequence.
CC using these sequences, the amplification of HIV nucleic acid
CC improved. The kits can also be used for the detection of other
CC microorganisms, by using different probe sequences. Other sequences
CC can be detected using this method include those from HBV (using the
CC sequences shown in T42410-T42412), and BCL-2 (using T42413-T42416).
CC samples can be clinical, environmental or forensic samples, and the
CC method produces large amounts of the target sequence for a variety of
CC uses. The method can also be used to produce multiple copies of a target
CC sequence for use in cloning, and sequencing, and to produce probes for
CC the target sequence.
SQ Sequence 50 BP; 17 A; 12 C; 11 G; 10 T;

Query Match 88.9%; Score 24; DB 28; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.07e-03;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Dn 27 actcagaccctgagctcaagtc 50
Cp 27 ACTCAGACCCTGAGCTCAAGTC 4

RESULT 4
ID Q86626 standard; DNA; 50 BP.
AC Q86626;
DE 15-NOV-1995 (first entry)
DE CML chromosomal translocation minus strand primer.
KW Primer; autocatalytic; target; CML; translocation; ss.
OS Synthetic.
PN US399491-A.
PD 21-MAR-1995.
PF 11-JUL-1989; 379501.
PR 11-JUL-1989; US-379501.
PR 10-JUL-1990; US-550837.
PR 19-MAR-1992; US-855732.
PA (GENP-) GEN-PROBE INC.
PI Fultz TJ, Kacian DL;
DE WPI; 95-130686/17.
PT Amplification of nucleic acid targets - using a reverse
PT transcriptase with RNase H activity and a RNA polymerase at
PT constant temp.
PS Disclosure; Column 9; 58pp; English.
CC Q86626-28 are primers and a probe for the CML chromosomal
CC translocation. They are used to produce autocatalytic
CC oligonucleotides which require no change in the experimental
CC conditions i.e. constant temperature, pH and ionic strength.
CC These sequences are useful in generating multiple copies of
CC specific nucleic acid target sequences.
SQ Sequence 50 BP; 17 A; 12 C; 11 G; 10 T;

Query Match 88.9%; Score 24; DB 15; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.07e-03;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Dn 27 actcagaccctgagctcaagtc 50
Cp 27 ACTCAGACCCTGAGCTCAAGTC 4

RESULT 5

ID 014244 standard; DNA: 22 BP.
AC 014244;
DT 20-JAN-1992 (first entry)
DE Primer CMLI.
KW Acute lymphocytic leukemia; chimeric; mRNA; ABL; breakpoint;
KW cluster; BCR; ABL; exon junction; PCR; ss.
OS Synthetic.
PN US5057410-A.
PD 15-OCT-1991.
PF 05-AUG-1988; 229604.
PR 05-AUG-1988; US-229604.
PA (CERTU) CERTUS CORP.
PI Kawasaki ES, McCormick EP, Wilto OO;
DR WPI: 91-324515/44.
PT Method for detecting chimeric mRNA - useful e.g. for
PT distinguishing between acute lymphocytic leukemia and chronic
PT myeloid leukemia.
PS Claim 5: Page 13; 14pp; English.
CC The primer is used with primer CMLI (014243) to amplify chimeric
CC mRNA contg. a specific exon-exon junction associated with chronic
CC myeloid leukemia (CML). It is complementary to cDNA sequences
CC within the ABL exon II. It can distinguish between ABL BCR-ABL
CC chimeric mRNA and CML BCR-ABL mRNA. The CML DNA sequences used
CC to design the primer are reported by Heisterkamp, N., et al.
CC Nucleu 315 (1985); Grosvelt, G., et al. Cell Biol. 6:607
CC (1987); and Shrivelman, E., et al. Cell 47:277 (1986).
CC See also 014241-47.
SQ Sequence 22 BP; 6 A; 7 C; 5 G; 4 T;

Query Match 81.5%; Score 22; DB 3; Length 22;
Best Local Similarity 100.0%; Pred. NO. 1,41e-02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 tcagaccctgagctcaagtc 22
|||||
Cp 25 TCAGACCTGAGCTCAAGTC 4

RESULT 6
ID 062302 standard; DNA: 22 BP.
AC 062302;
DT 02-NOV-1994 (first entry)
DE PCR primer for amplifying bcr/abl oncogene.
KW oncogene; amplification; polymerase chain reaction; PCR; blood;
KW reverse transcription; primer; ss.
OS Synthetic.
PN US5300635-A.
PD 05-APR-1994.
PF 01-FEB-1993; 013419.
PR 01-FEB-1993; US-013419.
PA (IOWA) UNIV IOWA STATE RES FOUND INC.
PI Macfarlane DE;
DR WPI: 94-125850/15.
PT Use of quaternary amine surfactants - for isolating nucleic acids
PT from a biological sample by forming complexes which can be
PT dissociated
PS Example 11: Column 11; 8pp; English.
CC Two primers (062302, 062303) were used to amplify the bcr/abl
CC oncogene. The amplification was performed to demonstrate that
CC isolation of RNA from whole blood by the cationic surfactant method
CC produces RNA which can be reverse transcribed and amplified without
CC the need for further purification.
SQ Sequence 22 BP; 6 A; 7 C; 5 G; 4 T;

Query Match 81.5%; Score 22; DB 10; Length 22;
Best Local Similarity 100.0%; Pred. NO. 1,41e-02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 tcagaccctgagctcaagtc 22
|||||
Cp 25 TCAGACCTGAGCTCAAGTC 4

RESULT 7
ID T88787 standard; DNA: 22 BP.
AC T88787;
DT 23-MAR-1998 (first entry)
DE Leukemic cell W-R-ABL target sequence detection probe.
KW Leukemia; BCR-ABL; cell line K562; target; immunosay; probe;
KW hybridisation; diagnostic; luciferase; genetic disease; ss.
OS Synthetic.
PN CA2186998-A.
PD 31-MAY-1997.
PF 02-OCT-1996; 185498.
PR 30-NOV-1995; US-565055.
PA (UYWI-) UNIV WINDSOR.
PI Christopoulos TK;
DR WPI: 97-415964/39.
PT Immunoassays and nucleic acid hybridisation assays - using
PT protein-encoding nucleic acid fragments as labels
PT Disclosure: Page 26; 39pp; English.
PS A novel assay has been developed for determining an analyte. The assay
CC comprises labelling the analyte with a nucleic acid fragment that
CC encodes a protein expressing the nucleic acid, and detecting the
CC protein. The present sequence represents a detection probe for a BCR-ABL
CC target sequence from a leukemic cell (cell line K562), used in an
CC example of the present assay. The assay is used for the determination
CC of antigens or nucleic acids for diagnostic or research purposes, e.g.
CC detecting low levels of tumour markers, analysing nucleic acid mutations
CC associated with genetic diseases, diagnosing and monitoring pathogen
CC infections, or searching for new disease markers. The immunosay when
CC using a luciferase for detection is more sensitive than an enzyme-
CC amplified, time-resolved fluorometric immunoassay and does not require
CC preparation of a luciferase-antibody conjugate.
SQ Sequence 22 BP; 6 A; 7 C; 5 G; 4 T;

Query Match 81.5%; Score 22; DB 36; Length 22;
Best Local Similarity 100.0%; Pred. NO. 1,41e-02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 tcagaccctgagctcaagtc 22
|||||
Cp 25 TCAGACCTGAGCTCAAGTC 4

RESULT 8
ID V01841 standard; DNA: 50 BP.
AC V01841;
DT 04-JUN-1998 (first entry)
DE PCR primer (ab15) used to produce antisense RNA and ribozyme sequences.
KW Antisense; inhibitor; gene expression; chromosomal translocation;
KW translocation point; pharmaceutical composition; bcr; bcr-abl;
KW chronic myelogenous leukemia; acute lymphoblastic leukemia;
KW acute myelogenous leukemia; Non-Hodgkin lymphoma; treatment;
KW PCR primer; amplify; ss.
OS Synthetic.
PN WO9746672-A2.
PD 11-DEC-1997.
PF 05-JUN-1997; EC0223.
PR 05-JUN-1996; EP0509034.
PA (DEKR-) DEUT KRYSFORSCHUNGSZENTRUM.
PI Haas R, Kronenwitt R, Szakiel G;
DR WPI: 98-042181/
PT Nucleic acid molecule containing chromosomal translocation point -
PT useful to treat chromosomal translocation disorders, e.g. chronic
PT myelogenous leukemia
PS Disclosure: Page 22; 49pp; English.
CC PCR primers V01841-7-43 were used to amplify bcr and bcr-abl sequences from
CC reverse transcribed mRNA isolated from the human Philadelphia-positive
CC (Ph+) cell line K562. The PCR products were used as a template for in
CC vitro synthesis of antisense RNA and ribozymes. Antisense molecules and
CC ribozymes are potent inhibitors of gene expression and vital functions.
CC The antisense molecules V01779-804 and the ribozymes V01805-32 exemplify
CC novel nucleic acid molecules of the invention. These nucleic acid
CC molecules contain portions complementary to a first and second
CC chromosomal DNA sequence. The nucleic acid molecule forms at least part

CC of a chromosomal translocation resulting in a fusion gene containing the
CC translocation point. The DNA sequence, as well as vectors and host cells
CC containing it are useful in pharmaceutical compositions for treating
CC disorders based on chromosomal translocations, preferably for chronic
CC myelogenous leukemia. The pharmaceutical composition may also be used
CC to treat acute lymphoblastic leukemias, acute myelogenous leukemias
CC and Non-Hodgkin lymphomas

SO Sequence 50 BP; 15 A; 14 C; 11 G; 10 T;
Query Match 74.1%; Score 20; DB 40; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.73e-01;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 31 actgagaccctgagctctaa 50
|||||
Cp 27 ACTGAGACCCTGAGCTCTAA 8

RESULT 9
ID V58784 standard; DNA; 24 BP.
AC V58784;
DT 10-DEC-1998 (first entry)
DE Detection probe for BCR/ABL type chimera mRNA.
KW Probe; BCR/ABL type chimera; chimera detection; Major-bcr;
KW nucleic acid strand based amplification; NASBA method; ss.
OS Synthetic.
PN J1029899-A.
PD 02-SEP-1998.
PE 21-FEB-1997; JP-054092.
PR 21-FEB-1997; JP-054092.
PA (SRLS-) SRL KK.
PA (TOYM-) TOYOBO KK.
DR WPI: 98-524294/45.
PT Forward side primer and reverse side primer - used for detection of
PT BCR/ABL type chimera mRNA easily with high sensitivity
PS Example 1; Page 6; 8pp; Japanese.
CC This sequence represents a probe for Major-bcr mRNA. The invention
CC relates to a method for the detection of a BCR/ABL type chimera mRNA with
CC a cleavage point in Major-bcr by using primers in a
CC nucleic acid strand based amplification (NASBA) method. The primers can
CC be used to detect BCR/ABL type chimera mRNA easily with high sensitivity.
SO Sequence 24 BP; 5 A; 6 C; 6 G; 7 T;

Query Match 70.4%; Score 19; DB 50; Length 24;
Best Local Similarity 68.4%; Pred. No. 5.93e-01;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
Db 6 tctgacttgagctcagc 24
||:||||:|||||
Cp 1 UCUGACUUGAGCCGCCAGG 19

RESULT 10
ID 086124 standard; RNA; 23 BP.
AC 086124;
DT 16-NOV-1995 (first entry)
DE bcr-abl mRNA junction fragment primer #2.
KW Catalytically active fragment; synthetic ribozyme subunit; neoplasm;
KW hybrid oncogene; chromosomal translocation; oncogene mRNA transcript;
KW flanking sequence; leukemia; bone marrow cell; PCR; primer; ss.
OS Synthetic.
PN WO9507923-A.
PD 23-MAR-1995.
PE 31-AUG-1994; U09963.
PR 15-SEP-1993; US-122795.
PA (UTEM) UNIV TEMPLE.
PI Leopold LH, Reddy EP, Reddy MVR, Shore SK;
DR WPI: 95-131308/17.
PT New multi-unit ribozyme which cleaves hybrid oncogene transcripts
PT - for treating neoplasms characterised by chromosomal
PS translocation(s), esp. leukemia
PS Example 7; Page 26; 44pp; English.
The sequences given in 086123-25 represent primers and a probe which

CC were used in the isolation of the bcr-abl mRNA. The isolated mRNA
CC was used to test the synthetic RNA molecule of the invention which is
CC useful for the treatment of neoplasm. The neoplasm to be treated is
CC characterised by the presence of a hybrid oncogene caused by
CC chromosomal translocation. The synthetic RNA molecule comprises at
CC least three ribozyme subunits each of which comprises a first
CC flanking sequence which has a nucleotide sequence complementary to
CC and hybridisable with the nucleotide sequence of a portion of the
CC oncogene mRNA transcript substantially 5' of the oncogene translocation
CC junction and a second flanking sequence which has a nucleotide sequence
CC complementary to, and hybridisable with, the nucleotide sequence of a
CC portion of the oncogene mRNA transcript substantially 3' of the oncogene
CC translocation junction and a catalytically active segment disposed
CC between the first and second flanking segments comprising a ribozyme
CC capable of cleaving the oncogene on or near the translocation junction.
CC The synthetic RNA's can be used to treat neoplasms, esp. leukemia. The
CC patients cells may be treated in vivo or cells, esp. bone marrow cells,
CC are aspirated, treated and returned to the patient.
SO Sequence 23 BP; 6 A; 7 C; 5 G; 5 T;

Query Match 63.0%; Score 17; DB 15; Length 23;
Best Local Similarity 94.7%; Pred. No. 6.51e-00;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 tcgagaccctgagctctaa 19
|||||
Cp 25 TCAGACCCTGAGCTCTCAA 7

RESULT 11
ID T62502 standard; DNA; 27 BP.
AC T62502;
DT 28-APR-1997 (first entry)
DE Murine retrovirus consensus right side integration response sequence.
KW Consensus sequence; right side; integration response; LTR;
KW long terminal repeat; retroviral attachment sequence; preparation;
KW gene delivery construct; ss.
OS Murine retrovirus.
PN WO9626745-A1.
PD 06-SEP-1996.
PE 28-FEB-1996; U02877.
PR 28-FEB-1996; US-395355.
PA (UYCR-) UNIV CREIGHTON.
PI Hodgson CP;
DR WPI: 96-412589/41.
PT Gene delivery system including liposome or dendrimer and
PT perpetuation molecule - esp. for gene therapy, provides efficient
PT and stable expression of chimeric genes more safely than use of
PT viruses.
PS Example 3; Fig 2; 50pp; English.
CC The present sequence is the murine retrovirus consensus right side
CC (U5) integration response sequence, which reads towards the cut site
CC of the long terminal repeat (LTR). It can be used as a retroviral
CC attachment sequence in the preparation of a gene delivery construct.
SO Sequence 27 BP; 1 A; 2 C; 0 G; 6 T;

Query Match 63.0%; Score 17; DB 28; Length 27;
Best Local Similarity 10.0%; Pred. No. 6.51e+00;
Matches 2; Conservative 16; Mismatches 2; Indels 0; Gaps 0;
Db 1 drvbsbshhhyvrrtc 20
||:||||:|||||
Cp 23 AGACCCTGAGCTCTAAAGTC 4

RESULT 12
ID T62502 standard; DNA; 27 BP.
AC T62502;
DT 28-APR-1997 (first entry)
DE Murine retrovirus consensus right side integration response sequence.
KW Consensus sequence; right side; integration response; LTR;
KW long terminal repeat; retroviral attachment sequence; preparation;
KW gene delivery construct; ss.

OS Murine retrovirus.
PN W09626745-A1.
PD 06-SEP-1996.
PF 28-FEB-1996; 002877.
PR 28-FEB-1995; US-395355.
PA (UYCR-) UNIV CREIGHTON.
PI Hodgson CP.
DR WPI: 96-412589/41.
PT Gene delivery system including liposome or dendrimer and perpetuation molecule - esp. for gene therapy, provides efficient and stable expression of chimeric genes more safely than use of viruses.
PS Example 3: Fig 2; 50pp; English.
CC The present sequence is the murine retrovirus consensus right side (U5) integration response sequence, which reads towards the outside of the long terminal repeat (LTR). It can be used as a retroviral attachment sequence in the preparation of a gene delivery construct.
CC Sequence 27 BP: 1 A; 2 C; 0 G; 6 T;
SQ

Query Match 59.3%; Score 16; DB 28; Length 27;
Best Local Similarity 4.8%; Pred. No. 2,08e+01;
Matches 1; Conservative 17; Mismatches 3; Indels 0; Gaps 0;

DB 1 drvbsbshbhyrrrrct 21
QY 3 ugacutugagccucagucuc 23

RESULT 13
ID T91968 standard; RNA; 16 BP.
AC T91968-1998 (first entry)
DE RNA sequence disclosed in patent on miniribozymes.
DR miniribozyme; ribozyme; dimer; cleavage; disease; treatment; ss.
KM Synthetic.
PN 009224673-A.
PD 02-SEP-1997.
PF 22-FEB-1996; 034898.
PR (AGEN) AGENCY OF IND SCI & TECHNOLOGY.
PA (HITB) HITACHI CHEM CO LTD.
PA (TAIS) TAIHO PHARM CO LTD.
DR WPI: 97-553198/51.
PT Two miniribozymes which hybridise to form a new heterodimer - useful for cleavage and inactivation of a target DNA, especially for diagnosis and treatment of genetic disease
PS Disclosure; Page 12; 15pp; Japanese.
CC The following mini-ribozymes of formulae (I) and (II) are new:
CC 3'-Rin...Q12 Q11 A A A G L V Q21 Q22...Q2m-5' (I); and
CC 3'-Rin...R12 R11 W M A G Y A G U C R21 R22...R2m-5' (II).
CC Y = A, G, C or U; L = (3')-C-(5'); N = A, U, G or C and
CC L = (3')-C NP-(5') and M = (3')-N'P G-(5'); P = 1-10 (same for both N and
CC N') = the complementary nucleotides of N; P = 1-10 (same for both N and
CC O and R are RNA or DNA mononucleotides complementary to a target RNA;
CC Q1n...Q12 Q11 with R1n...R12 R11 and Q21 Q22...Q2m with R21 R22...R2m
CC are same or different; m, n = an integer. Miniribozyme dimers of the
CC formula (I/II) are also claimed and have a two-part binding region for
CC target RNA and L and M are base-paired to form a stem structure. The
CC miniribozymes and the dimer they form can be used for cleavage and
CC inactivation of RNA. They are also useful as agents for treatment or
CC diagnosis of a genetic disease. The present sequence was disclosed
CC in the sequence ID listing of the specification.
SQ Sequence 16 BP: 2 A; 4 C; 6 G; 4 U;

Query Match 55.6%; Score 15; DB 35; Length 16;
Best Local Similarity 100.0%; Pred. No. 6,46e+01;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 ccucaggucucaguc 15
QY 13 CCUCAGGUCUCAGUC 27

RESULT 14
ID 051057 standard; DNA; 20 BP.
AC 051057;
DE 11-MAY-1994 (first entry)
DE Human glucokinase exon 1a PCR-SSCP analysis downstream primer.
KM Human; glucokinase; short arm; chromosome 7; MODY; insulin secretion;
KM non-insulin dependent diabetes mellitus; NIDDM; glucose-6-phosphate;
KM maturity-onset diabetes of the young; glucose; regulation; mutation;
KM detection; primary; amplify; single-strand conformational polymorphism;
KM adenosine deaminase; ADA; GLUT2; beta-cell glucose transporter;
KM restriction fragment length polymorphism; polymerase chain reaction;
KM RFLP; SSCP; exon; PCR; ss.
OS Synthetic.
PN W09321343-A.
PD 28-OCT-1993.
PF 14-APR-1993; 003560.
PR 22-APR-1992; US-872678.
PA (ARCH-) ARCH DEF CORP.
PI BEL GI; Cohen D; Firooz P; Pillels SJ; Stoffel M;
PI Takeda T; Velho G; Vionnet N; Yasuda K; Zouali H;
DR WPI: 93-351752/44.
PT Detection of early onset, non-insulin dependent diabetes mellitus by detecting a mutation in a glucokinase gene or prod., esp.
PT for maturity onset diabetes of the young
PS Example 7; Page 51; 60pp; English.
CC The sequences given in 051045-79 are primers which were used in the detection of restriction fragment length polymorphisms (RFLPs) within the human adenosine deaminase gene (ADA), beta-cell glucose transporter gene (GLUT2) and the human glucokinase gene. The glucokinase gene maps to a locus on the short arm of chromosome 7 and mutations within this gene show some correlation with certain forms of non-insulin dependent diabetes mellitus (NIDDM), esp. maturity onset diabetes of the young (MODY). The polymorphic AluVPA region of ADA cosegregates with one gene responsible for MODY and has been mapped to the long arm of chromosome 20. Glucokinase is an enzyme which catalyses the formation of glucose-6-phosphate from glucose and may be involved in the regulation of insulin secretion and integration of hepatic intermediary metabolism. Nonsense and missense mutations within the glucokinase gene (see also 051038-44) may be identified by the method of the invention. Early onset NIDDM is examined by detecting at least one single nucleotide change in a portion of the gene. The DNA is isolated and a pair of primers are selected which are capable of amplifying an exon of the gene via PCR. The single nucleotide changes are identified in the amplification product.
CC Sequence 20 BP: 6 A; 5 C; 4 G; 5 T;
SQ

Query Match 55.6%; Score 15; DB 9; Length 20;
Best Local Similarity 89.5%; Pred. No. 6,46e+01;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

DB 1 tccatctctgcgtcaaa 19
CP 25 TCAACCTGAGCCTCAAA 7

RESULT 15
ID V39479 standard; DNA; 20 BP.
AC V39479;
DE 22-SEP-1998 (first entry)
DE Chronic myelogenous/acute lymphocytic leukaemia detection probe.
DE Acute lymphocytic leukaemia/Chronic myelogenous leukaemia; ALL; CML;
KM target; capture probe; detection probe; hybridisation; bcr; abl;
KM multiple analysis; Salmonella; chromosomal translocation;
KM Philadelphia chromosome; ss.
OS Synthetic.
OS Homo sapiens.
PN EP-846776-A2.
PD 10-JUN-1998.
PF 05-DEC-1997; 304831.
PR 06-DEC-1996; US-761131.
PA (VYSI-) VYSIS INC.
PI Lane DJ, Muller JK;

DR WPI: 98-299988/27.
PT Assay device for isolating analyte from sample, e.g. Salmonella in
PT food - comprises tube containing linear array of binding elements,
PT linked to binding factor to which component binds
PS Example 2: Page 13: 25pp: English
CC An assay device has been developed for isolating an analyte from a
CC sample. The assay device comprises a tube containing a linear array of
CC binding elements, each linked to a distinct binding factor to which a
CC corresponding specific component binds, where each of the binding
CC elements is configured to sealingly contact the interior surface of the
CC tube along the entire circumference of the binding element. The present
CC sequence represents a detection probe used in an example from the present
CC invention for the detection of chromosomal translocations. The new
CC method and device can be used to detect e.g. Salmonella in a food
CC sample. They are also used to detect chromosomal translocations to
CC detect the 'Philadelphia' chromosome responsible for acute lymphocytic
CC leukaemia and chronic myelogenous leukaemia.
SQ Sequence 20 BP; 7 A; 4 C; 5 G; 4 T;

Query Match 55.6%; Score 15; DB 45; Length 20;
Best Local Similarity 60.0%; Pred. No. 6.46e+01;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 aggcctcaagtcaga 15
CP 15 AGGCTCAAGTCAGA 1

RESULT 16
ID V39474 standard; DNA; 40 BP.
AC V39474;
DT 22-SEP-1998 (first entry)
DE Chronic myelogenous leukaemia model target oligonucleotide.
KW Acute lymphocytic leukaemia; Chronic myelogenous leukaemia; ALL; CML;
KW target; capture probe; detection probe; hybridisation; bcr; abl;
KW multiple analyte; Salmonella; chromosomal translocation;
KW Philadelphia chromosome; ss.
OS Synthetic.
OS Homo sapiens.
PN EP-846776-A2.
PD 10-JUN-1998.
PF 05-DEC-1997; 309831.
PR 06-DEC-1996; US-761131.
PA (VXSI-) VXSIS INC.
PI Lane DJ, Muller UR;
DR WPI: 98-299988/27.
PT Assay device for isolating analyte from sample, e.g. Salmonella in
PT food - comprises tube containing linear array of binding elements,
PT linked to binding factor to which component binds
PS Example 2: Page 12: 25pp: English.
CC An assay device has been developed for isolating an analyte from a
CC sample. The assay device comprises a tube containing a linear array of
CC binding elements, each linked to a distinct binding factor to which a
CC corresponding specific component binds, where each of the binding
CC elements is configured to sealingly contact the interior surface of the
CC tube along the entire circumference of the binding element. The present
CC sequence represents a model target used in an example from the present
CC invention for the detection of chromosomal translocations. The new
CC method and device can be used to detect e.g. Salmonella in a food
CC sample. They are also used to detect chromosomal translocations to
CC detect the 'Philadelphia' chromosome responsible for acute lymphocytic
CC leukaemia and chronic myelogenous leukaemia.
SQ Sequence 40 BP; 10 A; 10 C; 8 G; 12 T;

Query Match 55.6%; Score 15; DB 45; Length 40;
Best Local Similarity 60.0%; Pred. No. 6.46e+01;
Matches 9; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Db 26 tctgactttgagcct 40
QY 1 UCUGACUUGAGCCU 15

RESULT 17
ID V39473 standard; DNA; 40 BP.
AC V39473;
DT 22-SEP-1998 (first entry)
DE Acute lymphocytic leukaemia model target oligonucleotide.
KW Acute lymphocytic leukaemia; Chronic myelogenous leukaemia; ALL; CML;
KW target; capture probe; detection probe; hybridisation; bcr; abl;
KW Philadelphia chromosome; ss.
OS Synthetic.
OS Homo sapiens.
PN EP-846776-A2.
PD 10-JUN-1998.
PF 05-DEC-1997; 309831.
PR 06-DEC-1996; US-761131.
PA (VXSI-) VXSIS INC.
PI Lane DJ, Muller UR;
DR WPI: 98-299988/27.
PT Assay device for isolating analyte from sample, e.g. Salmonella in
PT food - comprises tube containing linear array of binding elements,
PT linked to binding factor to which component binds
PS Example 2: Page 12: 25pp: English.
CC An assay device has been developed for isolating an analyte from a
CC sample. The assay device comprises a tube containing a linear array of
CC binding elements, each linked to a distinct binding factor to which a
CC corresponding specific component binds, where each of the binding
CC elements is configured to sealingly contact the interior surface of the
CC tube along the entire circumference of the binding element. The present
CC sequence represents a model target used in an example from the present
CC invention for the detection of chromosomal translocations. The new
CC method and device can be used to detect e.g. Salmonella in a food
CC sample. They are also used to detect chromosomal translocations to
CC detect the 'Philadelphia' chromosome responsible for acute lymphocytic
CC leukaemia and chronic myelogenous leukaemia.
SQ Sequence 40 BP; 10 A; 13 C; 7 G; 10 T;

Query Match 55.6%; Score 15; DB 45; Length 40;
Best Local Similarity 60.0%; Pred. No. 6.46e+01;
Matches 9; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Db 26 tctgactttgagcct 40
QY 1 UCUGACUUGAGCCU 15

RESULT 18
ID Q56492 standard; DNA; 48 BP.
AC Q56492;
DT 25-JUL-1994 (first entry)
DE PCR primer for K552 cell line used in 3SR amplification reaction.
KW PCR; polymerase chain reaction; amplification; detection;
KW translocation; point mutation; RNA; ribonucleic acid; in situ; ss.
OS Synthetic.
PN WO9402644-A.
PD 03-FEB-1994.
PF 16-JUL-1993; UO0716.
PR 17-JUL-1992; US-913694.
PR 17-JUL-1992; US-915893.
PR 17-JUL-1992; US-915900.
PR 17-JUL-1992; US-916183.
PR 17-JUL-1992; US-915927.
PR 17-JUL-1992; US-916068.
PA (ABRO-) APROGENEX INC.
PA (BAKT) BAXTER DIAGNOSTICS INC.
PA (TEXA) UNIV TEXAS SYSTEM.
PI Asgari N, Blicke M, Bresser J, Colvin D, Cubbage ML;
PI Haydock PV, Ju SC, Jurtsch R, Prashad N, Reading CL;
PI Weber WD;
DR WPI: 94-048901/06.
PT Detection of RNA in cells or viruses - by means of in-situ 3SR
PT amplification
PS Example 1; Page 48; 88pp: English.
CC The 3SR amplification procedure allows the detection of a target RNA

CC molecule in a biological entity i.e RNA detection within cells or
 CC viruses. The process is especially useful for detecting RNA
 CC molecules that only occur in cells that have undergone chromosomal
 CC translocation (especially tumour cells) and RNA molecules
 CC transcribed from point mutated DNA segments. Two primers (Q56491,
 CC Q56492) were used to amplify RNA from the K562 human chronic
 CC myelogenous leukaemia-blast crisis cell line for the subsequent
 CC detection of a translocation.
 SQ Sequence 48 BP; 14 A; 12 C; 10 G; 12 T;

Query Match 55.6%; Score 15; DB 10; Length 48;
 Best Local Similarity 100.0%; Pred. No. 5.46e+01;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 34 actcagaccctgag 48
 ||||||||||||||||
 Cp 27 ACTCAGACCCTGAG 13

RESULT 19
 ID T38971 standard; DNA; 29 BP.
 AC T38971.
 DT 29-MAY-1997 (first entry)
 DE Interleukin IL-3 3' PCR primer.
 KW Cytokine; expression profile; genital wart; interleukin 12; IL-12;
 KW tumour regression; adjuvant; polymerase chain reaction; PCR;
 KW condyloma acuminata; human papilloma virus; HPV-6; HPV-11; HPV16;
 KW HPV18; anogenital; cutaneous; laryngeal; oesophageal; cancer; ss.
 OS Synthetic.
 PN WO9629091-A1.
 PD 26-SEP-1996.
 PF 22-MAR-1996; G00686.
 PR 22-MAR-1995; GR-005784.
 PA (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.
 PI Scarfint CG Stanley MA;
 DR WPI: 96-442947/44.
 PT Use of interleukin-12 to treat papilloma virus-associated lesions
 PT esp. as a vaccine adjuvant with papilloma virus antigen for
 PS Immuno: therapy of warts or tumours
 PS Disclosure: Page 14; 32pp; English.
 CC RNA was extracted from genital lesions, reverse transcribed to
 CC cDNA and then the cDNA was used as the template for PCR
 CC amplification of various cytokines using the primers in T38964-
 CC T39005. To confirm the identity of amplified cDNA, digoxigenin-
 CC labelled probes specific for each cytokine (see T39006-T39021)
 CC were hybridised with Southern blots of amplified sequences. The
 CC expression profile for regressing and non-regressing warts was
 CC established and compared to cytokine expression patterns in normal
 CC cervical tissue. Results showed that interleukin 12 is barely
 CC expressed (if at all) in non-regressing warts, but is expressed in
 CC regressing warts. This suggests a central role for IL-12 in wart
 CC regression. It has been found that IL-12 can be used (especially
 CC as a vaccine adjuvant) for treating papilloma virus-associated
 CC lesions such as condyloma acuminata (anogenital warts) caused by
 CC human papilloma virus type 6 (HPV-6) and/or HPV-11 and more
 CC generally for treatment of tumours associated with HPV16 and HPV18
 CC infection e.g. anogenital, cutaneous, laryngeal and oesophageal
 CC cancers.
 SQ Sequence 29 BP; 7 A; 6 C; 9 G; 7 T;

Query Match 51.9%; Score 14; DB 29; Length 29;
 Best Local Similarity 85.0%; Pred. No. 1.94e+02;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 2 agatcgaggtctcaagtc 21
 ||||||||||||||||
 Cp 23 AGACCTGAGGCTCAAGTC 4

RESULT 20
 ID Q08506 standard; DNA; 21 BP.
 AC Q08506;
 DT 29-MAR-1992 (first entry)

DE Sequence of 3' probe, corresponding to a region encoding amino
 DE acids 123-130 of the mature protein of human interleukin-3
 DE (rhIL-3).
 KW Lymphokine; bone marrow proliferation; cytopenia therapy; ss.
 OS Homo sapiens.
 PN WO9001039-A.
 PD 08-FEB-1990.
 PF 14-JUN-1989; 002599.
 PR 20-JUL-1988; US-221699.
 PA (IMMU-) IMMUNEX CORP.
 PI Anderson DM, Cosman DJ, Price VL;
 DR WPI: 90-067162/79.
 PT Compens. contg. recombinant non-glycosylated human interleukin-3
 PT - has increased biological activity and binding affinity, for
 PS treating cytopenias
 PS Example: Page 10; 23pp; English.
 CC The inventors claim a pharmaceutical compsn. which contains an
 CC effective amt. of a recombinant human interleukin-3 protein analogue,
 CC rhIL-3, (Asp15, Asp70). The rhIL-3 analogue has AA SQ in R09326,
 CC and a diluent and 1 or more than 1 biological response modifier.
 CC The compsn. has a biological specific activity of equal to or more
 CC than 4.0 x 10 to the 7 mcg/mg in a human bone marrow proliferation
 CC assay, and a binding affinity for human monocyte IL-3 receptors of
 CC equal to or more than 4.0 x 10 to the 10 (M to the minus 1).
 SQ Sequence 21 BP; 5 A; 5 C; 7 G; 4 T;

Query Match 48.1%; Score 13; DB 3; Length 21;
 Best Local Similarity 100.0%; Pred. No. 5.64e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 7 gaggtctcaagtc 19
 ||||||||||||
 Cp 16 GAGGCTCAAGTC 4

RESULT 21
 ID Q10345 standard; DNA; 21 BP.
 AC Q10345;
 DT 10-APR-1991 (first entry)
 DE Probe to the human interleukin-3 gene.
 KW hIL-3; urticaria; granulopoesis; erythropoesis; thrombopoesis;
 KW neutropenia; anaemia; thrombocytopenia; ss.
 OS Homo sapiens.
 PN WO9100350-A.
 PD 10-JAN-1991.
 PF 13-JUN-1990; US-374667.
 PR 30-JUN-1989; US-374667.
 PA (IMMU-) IMMUNEX CORP.
 PI Urdal DL, Sassenfeld H;
 DR WPI: 91-036745/05.
 PT Non-glycosylated human interleukin-3 analog proteins - expressed
 PT by transformed yeast of Saccharomyces cerevisiae which do not
 PT give detectable urticaria
 PS Example A: Page 7; 18pp; English.
 CC Probes were used in the isolation of human IL-3, which was then
 CC expressed in a modified form, with a mutation in the
 CC N-glycosylation sites. The modified IL-3 does not result in
 CC urticaria or infiltration of mast cells and lymphocytes into the
 CC dermis. It stimulates granulopoesis, erythropoesis and
 CC thrombopoesis in vivo and may used to treat neutropenia, anaemia
 CC and thrombocytopenia.
 SQ Sequence 21 BP; 5 A; 5 C; 7 G; 4 T;

Query Match 48.1%; Score 13; DB 2; Length 21;
 Best Local Similarity 100.0%; Pred. No. 5.64e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 7 gaggtctcaagtc 19
 ||||||||||||
 Cp 16 GAGGCTCAAGTC 4

RESULT 22
ID Q42804 standard; cDNA; 21 BP.
AC Q42804;
DT 15-SEP-1993 (first entry)
DE Human IL-3 probe.
KW Mast cell growth factor; interleukin; haematopoietic progenitor cell;
KW bone marrow cell; proliferation; differentiation; functional activation;
KW peripheral blood leukocyte; circulating granulocyte; ss.
OS Synthetic.
PN W09310229-A.
PD 27-MAY-1993.
PF 19-NOV-1992; U09848.
PR 22-NOV-1991; US-79753.
PA (IMMUNEX CORP.
PI Williams DE.
DR WPI; 93-182546/22.
PT MGF-interleukin-3 fusion proteins having enhanced activity - used
PT for regulating immune and inflammatory responses
PS Example 1; Page 17; 4pp; English.
CC Two oligonucleotides were synthesised, with sequences complementary
CC to selected 5' and 3' sequences of the hmlt-3 gene. The 5' probe,
CC complementary to a sequence encoding part of the hmlt-3 leader, has
CC the sequence given in Q42803. The 3' probe, corresp. to a region
CC encoding amino acids 123-130 of the mature protein, has the
CC sequence given in Q42804.
SQ Sequence 21 BP; 5 A; 5 C; 7 G; 4 T;

Query Match 48.1%; Score 13; DB 7; Length 21;
Best Local Similarity 100.0%; Pred. No. 5.64e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 7 gagctcaagtc 19
|||||
16 GAGCTCAAGTC 4

CP 16 GAGCTCAAGTC 4

RESULT 23
ID T63590 standard; DNA; 22 BP.
AC T63590;
DT 01-JUL-1997 (first entry)
DE CD59 PCR primer used to screen human genomic DNA library.
KW Xenotransplantation; organ transplant; transgenic animal;
KW transgenic pig; transgenic mouse; antibody mediated rejection;
KW hyperacute rejection; CD59; complement inhibitor; primer; PCR;
KW polymerase chain reaction; bacteriophage pl. ss.
OS Synthetic.
PN W09712035-A2.
PD 03-APR-1997.
PF 23-SEP-1996; U15255.
PR 27-SEP-1995; US-004461.
PR 03-JUL-1996; US-675773.
PA (NEXT-) NEXTRAN.
PI Byrne GW, Diamond LE, Logan JS, Sharma A;
DR WPI; 97-22581/20.
PT Transgenic animals expressing antigen reducing enzyme and complement
PT inhibitor - used for production of materials suitable for human
PT transplantation having a reduced risk of rejection
PS Example 4.1; Page 107; 146pp; English.
CC Oligonucleotide pairs (T63589-98), designed from previously
CC published sequence data and corresponding to the 5' and 3' regions
CC of CD59, CD46 and CD55 genes, were used to screen, by PCR, a human
CC genomic library constructed in phage pl. The primer pair given in
CC T63589-90 yielded a 288 bp product located 1602 bp 5' of the
CC transcriptional start of the CD59 gene. Transgenic mouse and pig
CC lines conrg. selected pl clones were produced. Expression of
CC complement inhibitors such as CD59, CD46 (membrane cofactor
CC protein) and CD55 (decay accelerating factor) in the endothelial
CC cells of transgenic animals can generate material suitable for
CC transplantation to humans, suppressing complement activation and
CC thereby reducing immune reaction.
SQ Sequence 22 BP; 5 A; 4 C; 8 G; 5 T;

Query Match 48.1%; Score 13; DB 29; Length 22;

Best Local Similarity 58.8%; Pred. No. 5.64e+02;
Matches 10; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Db 5 atttgaggagcaggt 21
|||||
5 ACUUGAGCCCTCAGGGU 21

QY 5 ACUUGAGCCCTCAGGGU 21

RESULT 24
ID V42514 standard; DNA; 24 BP.
AC V42514;
DT 05-OCT-1998 (first entry)
DE PCR primer used to amplify the basic region and helix II DNA of RELAX.
KW Basic helix-loop-helix; BHLH; RELAX; Rat Embryonic Longitudinal Axis;
KW control; gene expression; transcriptional activator; targeting;
KW protein expression; central nervous system; CNS; treatment;
KW nervous system disorder; PCR primer; ss.
OS Synthetic.
PN Rattus sp.
PD W09827206-A2.
PD 25-JUN-1998.
PF 19-DEC-1997; F0-368.
PR 19-DEC-1996; FR-015651.
PA (RHON) RHONE-EXPLENC RORER SA.
PI Mallet J, Ravassard P, Icard-Lepkalns C;
DR WPI; 98-362775/24.
PT Basic helix-loop-helix polypeptide and related nucleic acid - with
PT transcriptional activity, for targeting expression of genes to
PT central nervous system and treatment of nervous disease
PS Example 1; Page 10; 28pp; French.
CC PCR primers V42513-14 are degenerate primers used to amplify DNA encoding
CC the basic domain and helix II of a basic helix-loop-helix (BHLH) type
CC protein, designated RELAX (Rat Embryonic Longitudinal Axis) protein.
CC The protein is used to control and participate in gene expression,
CC by acting as transcriptional activator, strictly dependent on the
CC presence of an intact E box (CANNTG), particularly for targeting
CC expression of proteins to the central nervous system (CNS). The
CC nucleic acid sequence can be used to treat nervous system disorders,
CC and antisense sequences can be used to control mRNA transcription.
SQ Sequence 24 BP; 2 A; 3 C; 6 G; 5 T;

Query Match 48.1%; Score 13; DB 46; Length 24;
Best Local Similarity 33.3%; Pred. No. 5.64e+02;
Matches 5; Conservative 9; Mismatches 1; Indels 0; Gaps 0;

Db 4 srtlytcagggtatyb 18
:::|||||
10 GAGCCTCAGGCTCUG 24

QY 10 GAGCCTCAGGCTCUG 24

RESULT 25
ID V95538 standard; RNA; 27 BP.
AC V95538;
DT 24-FEB-1999 (first entry)
DE Human c-fos hampered ribozyme nucleotide position 1267.
KW Human; c-fos; hampered ribozyme; hairpin ribozyme; target site;
KW cancer; oncogene; leukemia; neuroblastoma; diagnosis; genetic drift;
KW mutation; diseased cell; ss.
OS Synthetic.
PN Homo sapiens.
PD W09832846-A2.
PD 30-JUL-1998.
PF 20-JAN-1998; U01017.
PR 23-JAN-1997; US-037658.
PA (RIBO-) RIBOZYME PHARM INC.
PI Jarvis T, McSwigen JA, Stinchcomb DR;
DR WPI; 98-427942/26.
PT Enzymatic nucleic acid molecules which specifically cleave RNA
PT derived from a c-fos gene - useful for treating conditions related
PT to levels of c-fos, especially cancer
PS Claim 9; Page 52; 72pp; English.
CC The present invention describes an enzymatic nucleic acid molecule which
CC specifically cleaves RNA derived from a c-fos gene. V95540 to V95540

DE Probe for human D segments - DXp4.
 KW Rat; constant region; immunoglobulin; ss.
 OS Synthetic.
 PN WO9203918-A.
 PD 19-MAR-1992.
 PF 28-AUG-1991: U06185.
 PR 29-AUG-1990: US-574748.
 PR 31-AUG-1990: US-575962.
 PA (GENP-) GENPHARM INT INC.
 PI Lonberg N, Kay R;
 DR WPI; 92-113962/14.
 PT Immunoglobulin transgenes - for prodn. of heterologous
 PS non-rearranged and/or rearranged Ig chains
 PS Example 5; Page 55; 172pp; English.
 CC The probe was used to isolate phage clones contg. D segments from a
 CC human genomic library. The probe, along with probe DXp1 and DN4
 CC (Q23426.8) are specific for for diversity region sequences
 CC (Y. Ichihara, et al., (1988), EMBO J., 7: 4141-4150).
 CC See also Q23419-50 and Q22417-30.
 SQ Sequence 42 BP; 10 A; 11 C; 15 G; 6 T;
 DB 3 ctgaatgagagcctcagg 21
 QY 2 ctgacutugagccucaggg 20

Query Match 48.1%; Score 13; DB 3; Length 42;
 Best Local Similarity 68.4%; Pred. No. 5.64e+02;
 Matches 13; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

DE VI2519 standard; DNA; 42 BP.
 AC VI2519;
 DT 26-MAY-1998 (first entry)
 DE Probe DXp4 for human D segment.
 KW Transgenic mouse; human; immunoglobulin; heavy chain segment; J region;
 KW joining region; constant region; VH family; variable gene; gamma isotype;
 KW diversity gene; isotype switching sequence; mu isotype; Ig production;
 KW monoclonal antibody; Mab production; antigen; heavy chain isotype;
 KW antigenic stimulation; probe; ss.
 OS Synthetic.
 OS Homo sapiens.
 PN US5625126-A.
 PD 29-APR-1997.
 PF 07-DEC-1994: 352322.
 PR 29-DEC-1994: US-352322.
 PR 29-AUG-1990: US-574748.
 PR 31-AUG-1990: US-575962.
 PR 17-DEC-1991: US-810279.
 PR 05-FEB-1992: US-834539.
 PR 18-MAR-1992: US-853408.
 PR 23-JUN-1992: US-904058.
 PR 16-DEC-1992: US-990860.
 PR 26-APR-1993: US-053131.
 PR 22-JUL-1993: US-096762.
 PR 18-NOV-1993: US-155301.
 PR 03-DEC-1993: US-161739.
 PR 10-DEC-1993: US-165699.
 PR 09-MAR-1994: US-209741.
 PA (GENP-) GENPHARM INT INC.
 PI Kay RM, Lonberg N;
 DR WPI; 97-258277/23.
 PT Human antibody producing transgenic mouse - containing transgene
 PT comprising human V, D and J genes and sequences to provide isotype
 PT switching in lymphocytes
 PS Example 4; Column 52; 153pp; English.
 CC This sequence represents a probe for the human diversity (D) segments.
 CC The identified sequence is used in the plasmid pR3, which is
 CC used to develop the transgenic mouse of the invention. The transgenic
 CC mouse of the invention contains in its genome a transgene comprising in
 CC operable linkage human variable (V), diversity (D) and J genes, a human
 CC mu constant region gene (muCH), at least 2 different non-mu human CH
 CC genes and associated isotype switching sequences, where human mu and

CC gamma switch sequences are located in closer proximity to each other than
 CC in the naturally occurring human immunoglobulin (Ig) locus, and where in
 CC lymphocytes of the mouse the transgene undergoes productive VDJ
 CC rearrangement and mu to gamma isotype switching by recombination between
 CC the human mu and gamma sequences, so that the mouse produces a serum
 CC containing Ig of at least 3 human heavy chain isotypes in response to
 CC antigenic stimulation. The transgenic mice can be used to produce human
 CC Ig and monoclonal antibodies (Mab), which are specifically reactive with
 CC human antigens. The Mab can be used in therapeutic or diagnostic
 CC applications. The transgenic mice can produce human Mab of multiple
 CC isotypes by undergoing isotype switching.
 SQ Sequence 42 BP; 10 A; 11 C; 15 G; 6 T;
 DB 3 ctgaatgagagcctcagg 21
 QY 2 ctgacutugagccucaggg 20

Query Match 48.1%; Score 13; DB 3; Length 42;
 Best Local Similarity 68.4%; Pred. No. 5.64e+02;
 Matches 13; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Search completed: Mon Aug 2 12:00:55 1999
 Job time : 264 secs.

(TM)

Distribution rights by Oxford Molecular Ltd

n.a. database search, using Smith-Waterman algorithm

```
Mon Aug 2 12:04:54 1999; masPar time 5.00 seconds
```

t generated

1 UCUGACUUUGAGCCUCAGGUCUGAGU 27
AGACTGAACCTCGGAGTCCAGACTCA

AGACTGAACTCGGAGTCCCAGACTCA

Gap 10

Dbase 0; Query 0

137068 seqs, 35432894 bases x 2

Minimum Match 0%

	DB seq	length	50
Maximum			

n-issued

Mean 5.285; Variance 3.144; scale 1.681

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No
c	1	22	81.5	22	4	PCT-US94-0	Sequence 10, Applicant 2,20e+0
c	2	22	81.5	22	4	PCT-US94-0	Sequence 1, Applicant 2,20e+0
c	3	22	81.5	22	2	US-08-55-5	Sequence 1, Applicant 2,20e+0
c	4	22	81.5	22	1	US-08-01-3	Sequence 1, Applicant 2,20e+0
c	5	22	81.5	22	1	US-08-12-2	Sequence 10, Applicant 2,20e+0
c	6	15	55.6	20	1	US-07-87-1	Sequence 13, Applicant 1,55e+0
c	7	15	55.6	20	3	US-08-76-1	Sequence 7, Applicant 1,55e+0
c	8	15	55.6	40	3	US-08-76-1	Sequence 2, Applicant 1,55e+0
c	9	15	55.6	40	3	US-08-76-1	Sequence 1, Applicant 1,55e+0
c	10	11	48.1	27	4	PCT-US95-1	Sequence 13, Applicant 1,55e+0
c	11	13	48.1	33	3	US-08-46-3	Sequence 61, Applicant 1,55e+0
c	12	13	48.1	42	2	US-08-64-5	Sequence 25, Applicant 1,55e+0
c	13	13	48.1	42	2	US-08-03-3	Sequence 25, Applicant 1,55e+0
c	14	13	48.1	42	3	US-08-09-6	Sequence 25, Applicant 1,55e+0
c	15	13	48.1	42	4	PCT-US93-0	Sequence 17, Applicant 1,55e+0
c	16	13	48.1	42	4	US-07-84-4	Sequence 17, Applicant 1,55e+0
c	17	13	48.1	42	4	PCT-US92-1	Sequence 25, Applicant 1,55e+0
c	18	13	48.1	45	3	US-07-85-3	Sequence 25, Applicant 1,55e+0
c	19	13	48.1	45	3	US-08-39-9	Sequence 53, Applicant 1,55e+0

Note: Post-processor removed 961 summaries from list due to search parameters chosen

ALIGNMENTS

ID	RESULT	1
PC	PCT-US94-09963A-70 STANDARD; DNA; UNC; 22 BP.	
DT	xxxxxx	
AC		
CC	Sequence 10, Application PC/US9409963A	
CC	Sequence 10, Application PC/US9409963A	
CC	GENERAL INFORMATION:	
CC	TITLE OF INVENTION: MULTI-UNIT RIBOZYME	
CC	TITLE OF INVENTION: INHIBITION OF ONCOGENE EXPRESSION	
CC	NUMBER OF SEQUENCES: 11	
CC	CORRESPONDENCE ADDRESS:	
CC	ADDRESSEE: Seidel, Gonda, Lavorgna	
CC	ADDRESSEE: & Monaco, P.C.	
CC	STREET: Two Penn Center Plaza, Suite 1800	
CC	CITY: Philadelphia	
CC	STATE: Pennsylvania	
CC	COUNTRY: U.S.A.	
CC	ZIP: 19101	
CC	COMPUTER READABLE FORM:	
CC	MEDIUM TYPE: Diskette, 3.50 Inch, 720 Kb	
CC	COMPUTER: IBM PS/2	
CC	OPERATING SYSTEM: MS-DOS	
CC	SOFTWARE: wordperfect 5.1	
CC	CURRENT APPLICATION DATA:	
CC	APPLICATION NUMBER: PCT/US94/09963A	
CC	FILING DATE:	
CC	CLASSIFICATION:	
CC	PRIOR APPLICATION DATA:	
CC	APPLICATION NUMBER: 122,795	
CC	FILING DATE: 15 September 1993	
CC	ATTORNEY/AGENT INFORMATION:	
CC	NAME: Monico, Daniel A.	
CC	REGISTRATION NUMBER: 30,480	
CC	REFERENCE/CHECK NUMBER: 6056-192	
CC	TELECOMMUNICATION INFORMATION:	
CC	TELEPHONE: (215) 568-8383	
CC	TELEFAX: (215) 568-5549	
CC	TELEX: NO	
CC	INFORMATION FOR SEQ. ID NO.: 10:	
CC	SEQUENCE CHARACTERISTICS:	
CC	LENGTH: 21 Nucleotides	
CC	TYPE: nucleic acid	
CC	STRANDEDNESS: single stranded	
CC	TOPOLOGY: linear	
SEQ	SEQUENCE 22 BP, 6 A, 7 C, 5 G, 4 T, 0 OTHER.	
Query Match	81.5% Score 22, DB 4, Length 22;	

Best Local Similarity 100.0%; Pred. No. 2.20e-03;
Matches 22; Conservative 0; Mismatches 0; 1-2-3-4-5-6-7-8-9-10-11-12-13-14-15-16-17-18-19-20-21-22

Db 1 TCAGACCCCTGAGGCTCAAAGTC 22
|||||
Cp 25 TCAGACCCCTGAGGCTCAAAGTC 4

RESULT	2
ID	PCT-US94-00680-1 STANDARD; DNA; UNC; 22 BP.
AC	xxxxxx

CC APPLICANT: University of Iowa, Research Foundation
CC TITLE OF INVENTION: Quarternary Amine Surfactants and
CC TITLE OF INVENTION: Methods of Using Same in Isolation of RNA
CC NUMBER OF SEQUENCES: 2
CC CORRESPONDENCE ADDRESS:

CC ZIP: 19477
CC COMPUTER READABLE FORM:

CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC^c CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US94/00680
CC

MOLECULE TYPE: DNA (genomic)
SEQUENCE 22 BP; 6 A; 7 C; 5 G; 4 T; 0 OTHER.

bb 1 TCAGACCCCTGAGGCTCAAAGTC 22
|||
p 25 TCAGACCCCTGAGGCTCAAAGTC 4

RESULT 3
D US-08-525-818-1 STANDARD; DNA; UNC; 22 BP.
C

CC GENERAL INFORMATION:
CC APPLICANT: Macfarlane, Donald E.
CC TITLE OF INVENTION: Quaternary Amine Surfactants and Methods
CC TITLE OF INVENTION: of Using Same in Isolation of RNA
CC NUMBER OF SEQUENCES: 2
CC CORRESPONDENT ADDRESS:

CC COUNTRY: USA
CC ZIP: 19477
CC COMPUTER READABLE FORM:

CC SOFTWARE: PatentIn Release #1.0, Version #1.23
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/525,818
CC

Query Match	81.5%	Score 22;	DB 2;	Length 22;
Best Local Similarity	100.0%;	Pred. No. 2.20e-03;		
Matches	22;	Conservative	0;	Mismatches 0;

Db 1 TCAGACCCTGA.GGCTCAAAGTC 22
|||
Cp 25 TCAGACCCTGA.GGCTCAAAGTC 4

AC	RESULT	4
XXXXXX	US-08-013-419-1	STANDARD; DNA; UINC; 22 BP.

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

```

CC INFORMATION FOR SEQ ID NO: 10:
CC SEQUENCE CHARACTERISTICS
CC LENGTH: 22 Nucleotides
CC TYPE: nucleic acid
CC STRANDEDNESS: single stranded
CC TOPOLOGY: linear
CC SEQUENCE 22 BP: 6 A; 7 C; 5 G; 4 T; 0 OTHER.

Query Match 81.5%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 2,20e+03;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 TCAGACCTCGAGCTCAAGTC 22
|||||
CP 25 TCAGACCTCGAGCTCAAGTC 4

RESULT 6
ID US-07-872-678A-13 STANDARD; DNA; UNC; 20 BP.
AC xxxxxx
DT
Sequence 13, Application US/07872678A
Sequence 13, Application US/07872678A
CC Patent No. 5541060
CC GENERAL INFORMATION:
CC APPLICANT: Bell, Graeme, et al.
CC TITLE OF INVENTION: DETECTION OF EARLY-ONSET
CC TITLE OF INVENTION: NON-INSULIN-DEPENDENT DIABETES MELLITUS
CC NUMBER OF SEQUENCES: 48
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Arnold, White & Durkee
CC STREET: Post Office Box 4433
CC CITY: Houston
CC STATE: Texas
CC COUNTRY: USA
CC ZIP: 77210
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/07/872,678A
CC FILING DATE: 22-APRIL-1992
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Couglin, Daniel F.
CC REGISTRATION NUMBER: 36,111
CC REFERENCE/DOCKET NUMBER: ARCD016
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 713-787-1400
CC TELEFAX: 713-789-2679
CC TELEX: 79-0924
CC INFORMATION FOR SEQ ID NO: 13:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 20 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: DNA (genomic)
CC SEQUENCE 20 BP: 6 A; 5 C; 4 G; 5 T; 0 OTHER.

Query Match 55.6%; Score 15; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 1.56e+01;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 1 TCGATTCTGAGGCTCAA 19
|||||
CP 25 TCAGACCTCGAGGCTCAA 7

```

AC xxxxxx
DE Sequence 7, Application US/08761131
CC Sequence 7, Application US/08761131
CC Patent No. 5804384
CC GENERAL INFORMATION:
CC APPLICANT: M Iler, Uwe R. et al.
CC TITLE OF INVENTION: DEVICES AND METHODS FOR DETECTING
CC TITLE OF INVENTION: MULTIPLE ANALYTES IN SAMPLES
CC NUMBER OF SEQUENCES: 7
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Vysis, Inc.
CC STREET: 3100 Woodcreek Drive
CC CITY: Downers Grove
CC STATE: Illinois
CC COUNTRY: U.S.A.
CC ZIP: 60515
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Diskette
CC OPERATING SYSTEM: DOS
CC SOFTWARE: FASTSEQ Version 2.0
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/761,131
CC FILING DATE:
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER:
CC FILING DATE:
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Galloway, No. 5804384val B.
CC REGISTRATION NUMBER: 33,595
CC REFERENCE/DOCKET NUMBER: 01886/064001
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 708-271-7417
CC TELEFAX: 708-271-7048
CC TELEX: 200154
CC INFORMATION FOR SEQ ID NO: 7:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 20 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: Genomic DNA
CC SEQUENCE 20 BP; 7 A; 4 C; 5 G; 4 T; 0 OTHER.
SQ
Query Match 55.6%; Score 15; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.56e+01;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 1 AGGCTCAAGTCAGA 15
CP 15 AGGCTCAAGTCAGA 1
RESULT 8
ID US-08-761-131-2 STANDARD; DNA; UNC; 40 BP.
AC xxxxxx
DE Sequence 2, Application US/08761131
CC Sequence 2, Application US/08761131
CC Patent No. 5804384
CC GENERAL INFORMATION:
CC APPLICANT: M Iler, Uwe R. et al.
CC TITLE OF INVENTION: DEVICES AND METHODS FOR DETECTING
CC TITLE OF INVENTION: MULTIPLE ANALYTES IN SAMPLES
CC NUMBER OF SEQUENCES: 7
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Vysis, Inc.
CC STREET: 3100 Woodcreek Drive
CC CITY: Downers Grove
CC STATE: Illinois
CC COUNTRY: U.S.A.

CC ZIP: 60515
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Diskette
CC OPERATING SYSTEM: DOS
CC SOFTWARE: FASTSEQ Version 2.0
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/761,131
CC FILING DATE:
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER:
CC FILING DATE:
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Galloway, No. 5804384val B.
CC REGISTRATION NUMBER: 33,595
CC REFERENCE/DOCKET NUMBER: 01886/064001
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 708-271-7417
CC TELEFAX: 708-271-7048
CC TELEX: 200154
CC INFORMATION FOR SEQ ID NO: 2:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 40 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: Genomic DNA
CC SEQUENCE 40 BP; 10 A; 10 C; 8 G; 12 T; 0 OTHER.
SQ
Query Match 55.6%; Score 15; DB 3; Length 40;
Best Local Similarity 60.0%; Pred. No. 1.56e+01;
Matches 9; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
DB 26 TCGACCTTGAGCCT 40
CY 1 TCGACCTTGAGCCT 15
RESULT 9
ID US-08-761-131-1 STANDARD; DNA; UNC; 40 BP.
AC xxxxxx
DE Sequence 1, Application US/08761131
CC Sequence 1, Application US/08761131
CC Patent No. 5804384
CC GENERAL INFORMATION:
CC APPLICANT: M Iler, Uwe R. et al.
CC TITLE OF INVENTION: DEVICES AND METHODS FOR DETECTING
CC TITLE OF INVENTION: MULTIPLE ANALYTES IN SAMPLES
CC NUMBER OF SEQUENCES: 7
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Vysis, Inc.
CC STREET: 3100 Woodcreek Drive
CC CITY: Downers Grove
CC STATE: Illinois
CC COUNTRY: U.S.A.
CC ZIP: 60515
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Diskette
CC OPERATING SYSTEM: DOS
CC SOFTWARE: FASTSEQ Version 2.0
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/761,131
CC FILING DATE:
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER:
CC FILING DATE:
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Galloway, No. 5804384val B.
CC REGISTRATION NUMBER: 33,595

REFERENCE/DOCKET NUMBER: 01886/064001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-271-7417
TELEFAX: 708-271-7048
TELEX: 200154
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
SEQUENCE 40 BP; 10 A; 13 C; 7 G; 10 T; 0 OTHER.

Query Match 55.6%; Score 15; DB 3; Length 40;
Best Local Similarity 60.0%; Pred. No. 1.56e+01;
Matches 9; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Db 26 TCTGACTTGAGCCT 40
1 UCUGACUUGAGCCU 15

RESULT 10
ID PCT-US95-13041-13 STANDARD: DNA; UNC; 27 BP.
AC xxxxxx
DE Sequence 13, Application PC/US9513041
Sequence 13, Application PC/US9513041
GENERAL INFORMATION:
APPLICANT: WHITE, Morris F.
APPLICANT: SUN, Xiao Jian
APPLICANT: PIERCE, Jacalyn H.
TITLE OF INVENTION: THE IRS FAMILY OF GENES
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESSES:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/13041
FILING DATE: Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/317,310
FILING DATE: 03-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Louis Myers
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: JDP-022PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-5941
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE 27 BP; 7 A; 10 C; 6 G; 3 T; 1 OTHER.

Query Match 48.1%; Score 13; DB 4; Length 27;
Best Local Similarity 86.7%; Pred. No. 1.55e+02;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 11 ACCCARACCTGAGG 25
11 |||||
Cp 27 ACTGAGACCTGAGG 13

RESULT 11
ID US-08-463-224-61 STANDARD: DNA; UNC; 33 BP.
AC xxxxxx
DE Sequence 61, Application US/08463224
Sequence 61, Application US/08463224
Patent No. 5807824
GENERAL INFORMATION:
APPLICANT: van Oostrum, Jan
APPLICANT: Royer, William C.
APPLICANT: Galakatos, Nicholas G.
APPLICANT: Schmitz, Albert
APPLICANT: van Hecke, Gino
TITLE OF INVENTION: G5a Receptor Antagonists Having
TITLE OF INVENTION: Substantially No. 5807824agonist Activity
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Lerner, David, Littenberg, Krumholz & Mentlik
STREET: 600 South Avenue West
CITY: Westfield
STATE: NJ
COUNTRY: USA
ZIP: 07090
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,224
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Foley, Sharrn P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-654-5000
TELEFAX: 908-654-7866
TELEX: 139-125
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE 33 BP; 11 A; 6 C; 9 G; 7 T; 0 OTHER.

Query Match 48.1%; Score 13; DB 3; Length 33;
Best Local Similarity 88.2%; Pred. No. 1.55e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 12 CAGACATGAGCTCAA 28
11 |||||
Cp 24 CAGACCTGAGCTCAA 8

RESULT 12
ID US-08-645-641-25 STANDARD: DNA; UNC; 42 BP.
AC xxxxxx
DE Sequence 25, Application US/08645641
Sequence 25, Application US/08645641
Patent No. 5719032
GENERAL INFORMATION:
APPLICANT: Loberg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 5719032-Human Animals for
TITLE OF INVENTION: Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 150

```
CC      PRIOR APPLICATION DATA:  
CC      APPLICATION NUMBER: US 07/990,860  
CC      FILING DATE: 16-DEC-1992  
CC      PRIOR APPLICATION DATA:  
CC      APPLICATION NUMBER: US 07/810,279  
CC      FILING DATE: 17-DEC-1991  
CC      PRIOR APPLICATION DATA:  
CC      APPLICATION NUMBER: US 07/853,408  
CC      FILING DATE: 18-MAR-1992  
CC      ATTORNEY/AGENT INFORMATION:  
CC      NAME: Smith, William M.  
CC      REGISTRATION NUMBER: 30,223  
CC      REFERENCE/DOCKET NUMBER: 14643-9-3  
CC      TELECOMMUNICATION INFORMATION:  
CC      TELEPHONE: 415-326-2400  
CC      TELEFAX: 415-326-2422  
CC      INFORMATION FOR SEQ ID NO.: 25:  
CC      SEQUENCE CHARACTERISTICS:  
CC          LENGTH: 42 base pairs  
CC          TYPE: nucleic acid  
CC          STRANDEDNESS: single  
CC          TOPOLOGY: linear  
CC      MOLECULE TYPE: DNA (primer)  
CC      SEQUENCE 42 BP; 10 A; 11 C; 15 G; 6 T; 0 OTHER.
```

DQ

```
DB       3 CTGCAATGGACCTTAGGG 21  
         ||||| : |||||||:|||||  
OY       2 CGAGCUCUGGCCUCCGCGG 20
```

RESULT 14

```
ID   US-08-096-762-25 STANDARD. DNA; UNC; 42 BP.  
AC    xxxxxx
```

DE Sequence 25, Application US/08096762
CC Sequence 25, Application US/08096762
CC Patent No. 5814318
CC GENERAL INFORMATION:
CC APPLICANT: Lomborg, Nils
CC APPLICANT: Kay, Robert W.
CC TITLE OF INVENTION: Transgenic No. 5814318-Human Animals for
CC TITLE OF INVENTION: Producing Heterologous Antibodies
CC NUMBER OF SEQUENCES: 210
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Townsend and Townsend Kourie and Crew
CC STREET: One Market Plaza, Steuart Tower, Suite 200
CC CITY: San Francisco
CC STATE: California
CC COUNTRY: USA
CC ZIP: 94105
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC OPERATING SYSTEM: IBM PC compatible
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/0956,762
CC FILING DATE: 22-JUN-1993
CC CLASSIFICATION: 800
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/053,131
CC FILING DATE: 26-APR-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/990,860
CC FILING DATE: 16-DEC-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/904,068
CC FILING DATE: 23-JUN-1992
CC PRIOR APPLICATION DATA:

CC	APPLICATION NUMBER:	US 07/953,408
CC	FILING DATE:	18-MAR-1992
CC	PRIOR APPLICATION DATA:	
CC	APPLICATION NUMBER:	US 07/810,279
CC	FILING DATE:	17-DEC-1991
CC	ATTORNEY/AGENT INFORMATION:	
CC	NAME:	Smith, William M.
CC	REGISTRATION NUMBER:	30,223
CC	REFERENCE/DOCKET NUMBER:	14643-9-4
CC	TELECOMMUNICATION INFORMATION:	
CC	TELEPHONE:	415-326-2400
CC	TELEFAX:	415-326-2422
CC	INFORMATION FOR SEQ ID NO:	25;
CC	SEQUENCE CHARACTERISTICS:	
CC	LENGTH:	42 base pairs
CC	TYPE:	nucleic acid
CC	STRANDEDNESS:	single
CC	TOPOLOGY:	linear
CC	MOLECULE TYPE:	DNA (primer)
SQ	SEQUENCE 42 BP:	10 A; 11 C; 15 G; 6 T; 0 OTHER.
DB	Query Match	48.1%; Score 13; DB 3; Length 42;
CC	Best Local Similarity	68.4%; Pred. No. 1.55e+02;
OY	Matches 13; Conservative	3; Mismatches 3; Indels 0; Gaps 0;
DB	3 CTGAATGAGCCTCAGGG 21	
CC	1:11 : 11111:11111	
CC	2 CUGACUUGAGCCUCACAGG 20	
CC	COUNTRY: USA	
CC	ZIP: 94105	
CC	COMPUTER READABLE FORM:	
CC	MEDIUM TYPE:	Floppy disk
CC	COMPUTER:	IBM PC compatible
CC	OPERATING SYSTEM:	PC-DOS/MS-DOS
CC	SOFTWARE:	Patentin Release #1.0, Version #1.25
CC	CURRENT APPLICATION DATA:	
CC	APPLICATION NUMBER:	PCT/US92/06185
CC	FILING DATE:	19910828
CC	CLASSIFICATION:	
CC	ATTORNEY/AGENT INFORMATION:	
CC	NAME:	Smith, William M.
CC	REGISTRATION NUMBER:	87654
CC	REFERENCE/DOCKET NUMBER:	14643-5
CC	TELECOMMUNICATION INFORMATION:	
CC	TELEPHONE:	415-543-9600
CC	TELEFAX:	415-543-5043
CC	INFORMATION FOR SEQ ID NO:	17;
CC	SEQUENCE CHARACTERISTICS:	
CC	LENGTH:	42 base pairs
CC	TYPE:	nucleic acid
CC	STRANDEDNESS:	single
CC	TOPOLOGY:	linear
CC	MOLECULE TYPE:	DNA (genomic)
SQ	SEQUENCE 42 BP:	10 A; 11 C; 15 G; 6 T; 0 OTHER.
DB	Query Match	48.1%; Score 13; DB 1; Length 42;
CC	Best Local Similarity	68.4%; Pred. No. 1.55e+02;
OY	Matches 13; Conservative	3; Mismatches 3; Indels 0; Gaps 0;
DB	3 CTGAATGAGCCTCAGGG 21	
CC	1:11 : 11111:11111	
CC	2 CUGACUUGAGCCUCACAGG 20	
CC	COUNTRY: USA	
CC	ZIP: 94105	
CC	COMPUTER READABLE FORM:	
CC	MEDIUM TYPE:	Floppy disk
CC	COMPUTER:	IBM PC compatible
CC	OPERATING SYSTEM:	PC-DOS/MS-DOS
CC	SOFTWARE:	Patentin Release #1.0, Version #1.25
CC	CURRENT APPLICATION DATA:	
CC	APPLICATION NUMBER:	US/07/834,539A
CC	FILING DATE:	1992-02-05
CC	CLASSIFICATION:	
CC	ATTORNEY/AGENT INFORMATION:	
CC	NAME:	Smith, William M.
CC	REGISTRATION NUMBER:	30,223
CC	REFERENCE/DOCKET NUMBER:	14643-5
CC	TELECOMMUNICATION INFORMATION:	
CC	TELEPHONE:	415-543-5043
CC	TELEFAX:	415-543-5043
CC	INFORMATION FOR SEQ ID NO:	17;
CC	SEQUENCE CHARACTERISTICS:	
CC	LENGTH:	42 base pairs
CC	TYPE:	nucleic acid
CC	STRANDEDNESS:	single
CC	TOPOLOGY:	linear
CC	MOLECULE TYPE:	DNA (genomic)
SQ	SEQUENCE 42 BP:	10 A; 11 C; 15 G; 6 T; 0 OTHER.
DB	Query Match	48.1%; Score 13; DB 1; Length 42;
CC	Best Local Similarity	68.4%; Pred. No. 1.55e+02;
OY	Matches 13; Conservative	3; Mismatches 3; Indels 0; Gaps 0;
DB	3 CTGAATGAGCCTCAGGG 21	
CC	1:11 : 11111:11111	
CC	2 CUGACUUGAGCCUCACAGG 20	
CC	COUNTRY: USA	
CC	ZIP: 94105	
CC	COMPUTER READABLE FORM:	
CC	MEDIUM TYPE:	Floppy disk
CC	COMPUTER:	IBM PC compatible
CC	OPERATING SYSTEM:	PC-DOS/MS-DOS
CC	SOFTWARE:	Patentin Release #1.0, Version #1.25
CC	CURRENT APPLICATION DATA:	
CC	APPLICATION NUMBER:	US/07/834,539A
CC	FILING DATE:	1992-02-05
CC	CLASSIFICATION:	
CC	ATTORNEY/AGENT INFORMATION:	
CC	NAME:	Smith, William M.
CC	REGISTRATION NUMBER:	30,223
CC	REFERENCE/DOCKET NUMBER:	14643-5
CC	TELECOMMUNICATION INFORMATION:	
CC	TELEPHONE:	415-543-5043
CC	TELEFAX:	415-543-5043
CC	INFORMATION FOR SEQ ID NO:	17;
CC	SEQUENCE CHARACTERISTICS:	
CC	LENGTH:	42 base pairs
CC	TYPE:	nucleic acid
CC	STRANDEDNESS:	single
CC	TOPOLOGY:	linear
CC	MOLECULE TYPE:	DNA (genomic)
SQ	SEQUENCE 42 BP:	10 A; 11 C; 15 G; 6 T; 0 OTHER.
DB	Query Match	48.1%; Score 13; DB 1; Length 42;
CC	Best Local Similarity	68.4%; Pred. No. 1.55e+02;
OY	Matches 13; Conservative	3; Mismatches 3; Indels 0; Gaps 0;
DB	3 CTGAATGAGCCTCAGGG 21	
CC	1:11 : 11111:11111	
CC	2 CUGACUUGAGCCUCACAGG 20	
CC	COUNTRY: USA	
CC	ZIP: 94105	
CC	COMPUTER READABLE FORM:	
CC	MEDIUM TYPE:	Floppy disk
CC	COMPUTER:	IBM PC compatible
CC	OPERATING SYSTEM:	PC-DOS/MS-DOS
CC	SOFTWARE:	Patentin Release #1.0, Version #1.25
CC	CURRENT APPLICATION DATA:	
CC	APPLICATION NUMBER:	US/07/834,539A
CC	FILING DATE:	1992-02-05

CC APPLICANT: Tai, Rony
CC APPLICANT: Wong, Hing C.
CC APPLICANT: Casipit, Clayton
CC APPLICANT: Chavalliaz, Pierre-Andre
CC APPLICANT: Wiltman, Vaughan
CC TITLE OF INVENTION: Methods for Peptide Synthesis and
CC TITLE OF INVENTION: Purification
CC NUMBER OF SEQUENCES: 57
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: DADE INTERNATIONAL, INC.
CC STREET: 1717 Deerfield Road
CC CITY: Deerfield
CC STATE: Illinois
CC COUNTRY: US
CC ZIP: 60015
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/428,733A
CC FILING DATE: 04-APR-1995
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/235,178
CC FILING DATE: 29-APR-1994
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Pearson, Louise S.
CC REGISTRATION NUMBER: 32,369
CC REFERENCE/DOCKET NUMBER: DA-4623 CIP
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (708) 267-5300
CC TELEFAX: (708) 267-5376
CC INFORMATION FOR SEQ ID NO: 7:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 37 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: unknown
CC TOPOLOGY: unknown
CC SEQ SEQUENCE 37 BP; 7 A; 9 C; 13 G; 8 T; 0 OTHER.
Query Match 44.4%; Score 12; DB 3; Length 37;
Best Local Similarity 75.0%; Pred. No. 4.61e+02;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Db 2 ACTCTGACGCTGAGCTGAGGTC 25
Cp 27 ACTGAGACCTGAGGCTCAAGTC 4
RESULT 23
ID US-08-428-733A-38 STANDARD; DNA; UNC; 37 BP.
DT xxxxxx
DE Sequence 38, Application US/08428733A
CC Sequence 38, Application US/08428733A
CC Patent No. 5763284
CC GENERAL INFORMATION:
CC APPLICANT: Tai, Rony
CC APPLICANT: Wong, Hing C.
CC APPLICANT: Casipit, Clayton
CC APPLICANT: Chavalliaz, Pierre-Andre
CC APPLICANT: Wiltman, Vaughan
CC TITLE OF INVENTION: Methods for Peptide Synthesis and
CC TITLE OF INVENTION: Purification
CC NUMBER OF SEQUENCES: 57
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: DADE INTERNATIONAL, INC.
CC STREET: 1717 Deerfield Road
CC CITY: Deerfield
CC STATE: Illinois
CC COUNTRY: US

CC ZIP: 60015
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/428,733A
CC FILING DATE: 04-APR-1995
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/235,178
CC FILING DATE: 29-APR-1994
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Pearson, Louise S.
CC REGISTRATION NUMBER: 32,369
CC REFERENCE/DOCKET NUMBER: DA-4623 CIP
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (708) 267-5300
CC TELEFAX: (708) 267-5376
CC INFORMATION FOR SEQ ID NO: 38:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 37 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: unknown
CC TOPOLOGY: unknown
CC SEQ SEQUENCE 37 BP; 7 A; 8 C; 14 G; 8 T; 0 OTHER.
Query Match 44.4%; Score 12; DB 3; Length 37;
Best Local Similarity 75.0%; Pred. No. 4.61e+02;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Db 7 ACTCTGACGCTGAGCTGAGGTC 30
Cp 27 ACTGAGACCTGAGGCTCAAGTC 4
RESULT 24
ID PCT-US95-07201-19 STANDARD; DNA; UNC; 24 BP.
DT xxxxxx
DE Sequence 19, Application PC/TUS9507201
CC Sequence 19, Application PC/TUS9507201
CC GENERAL INFORMATION:
CC APPLICANT: Chader, Gerald J.; Becerra, Sofia
CC APPLICANT: Patricia, Schwartz, Joan P.;
CC APPLICANT: Tanikawa, Takayuki
CC TITLE OF INVENTION: DERIVED FACTOR: CHARACTERIZATION GENOMIC
CC TITLE OF INVENTION: ORGANIZATION AND SEQUENCE OF THE PEDF GENE
CC NUMBER OF SEQUENCES: 43
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Morgan & Flinnegan, L.L.P.
CC STREET: 345 Park Avenue
CC CITY: New York
CC STATE: New York
CC COUNTRY: USA
CC ZIP: 10154
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: WORDPERFECT 5.1
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US95/07201
CC FILING DATE: 06-JUN-1995
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 08/367,841
CC FILING DATE: 30-DEC-1994
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 08/257,963
CC FILING DATE: 07-JUN-1994

CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 07/952,796
CC FILING DATE: 24-SEP-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: DOROTHY R. AUTH
CC REGISTRATION NUMBER: 36434
CC REFERENCE/DOCKET NUMBER: 20264126PCT
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (212) 751-6849
CC TELEFAX: (212) 751-6849
CC INFORMATION FOR SEQ ID NO: 19:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 24 base pairs
CC TYPE: Nucleic Acid
CC STRANDEDNESS: Unknown
CC TOPOLOGY: Unknown
CC MOLECULE TYPE: Oligonucleotide
CC FEATURE:
CC NAME/KEY: 2238
CC LOCATION:
CC IDENTIFICATION METHOD:
CC OTHER INFORMATION: primer in a polymerase
CC OTHER INFORMATION: chain reaction
CC
SQ SEQUENCE 24 BP; 5 A; 5 C; 7 G; 7 T; 0 OTHER.
Query Match 40.7%; Score 11; DB 4; Length 24;
Best Local Similarity 86.7%; Pred. No. 1.31e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Db 7 TCGAGCCCTGAGCT 21
11 ||||| |||||
Cp 25 TCGAGCCCTGAGCT 11
RESULT 25
ID US-07-999-280A-20 STANDARD; DNA; UNC; 25 BP.
AC xxxxxx
DE Sequence 20, Application US/07999280A
CC Sequence 20, Application US/07999280A
CC Patent No. 573930
CC GENERAL INFORMATION:
CC APPLICANT: LADNER, MARTHA B.
CC APPLICANT: NOBLE, JANELLE A.
CC APPLICANT: MARTIN, GEORGE S.
CC APPLICANT: KAWASAKI, ERNEST S.
CC APPLICANT: COYNE, MAZIE YEE
CC APPLICANT: HALENECK, ROBERT F.
CC APPLICANT: KOTHS, KIRSTON E.
CC TITLE OF INVENTION: NEW FORMS OF COLONY STIMULATING FACTOR-1
CC NUMBER OF SEQUENCES: 24
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: CHIRON CORPORATION
CC STREET: Intellectual Property - R440, P.O. Box 8097
CC CITY: Emeryville
CC STATE: California
CC COUNTRY: U.S.A.
CC ZIP: 94662-8097
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/07/999,280A
CC FILING DATE: 28-DEC-1992
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: McGarrigle, J., Philip L.
CC REGISTRATION NUMBER: 31,395
CC REFERENCE/DOCKET NUMBER: 0681.007
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (510) 601-2718

CC TELEFAX: (510) 655-3542
CC
CC INFORMATION FOR SEQ ID NO: 20:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 25 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: DNA (genomic)
CC SEQUENCE 25 BP; 5 A; 6 C; 8 G; 6 T; 0 OTHER.
Query Match 40.7%; Score 11; DB 1; Length 25;
Best Local Similarity 92.3%; Pred. No. 1.31e+03;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Db 13 TCGAGCTGAGG 25
11 ||||| |||||
Cp 25 TCGAGCTGAGG 13
RESULT 26
ID US-08-758-306-426 STANDARD; DNA; UNC; 27 BP.
AC xxxxxx
DE Sequence 426, Application US/08758306
CC Sequence 426, Application US/08758306
CC Patent No. 5807743
CC GENERAL INFORMATION:
CC APPLICANT: Slonchcomb, Dan T.
CC APPLICANT: McSwiggen, James A.
CC TITLE OF INVENTION: METHOD AND REAGENT FOR THE
CC TITLE OF INVENTION: TREATMENT OF DISEASES
CC TITLE OF INVENTION: ASSOCIATED WITH
CC TITLE OF INVENTION: INTERLEUKIN-2 RECEPTOR
CC TITLE OF INVENTION: GAMMA-CHAIN EXPRESSION
CC NUMBER OF SEQUENCES: 1379
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Lyon & Lyon
CC STREET: 633 West Fifth Street
CC CITY: Los Angeles
CC STATE: California
CC COUNTRY: U.S.A.
CC ZIP: 90071-2066
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: 3.5" Diskette, 1.44 MB
CC MEDIUM TYPE: storage
CC OPERATING SYSTEM: IBM P.C. DOS 5.0
CC SOFTWARE: FastSeq Version 1.5
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/758,306
CC FILING DATE: December 3, 1996
CC CLASSIFICATION: 514
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER:
CC FILING DATE:
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Warburg, Richard J.
CC REGISTRATION NUMBER: 32,327
CC REFERENCE/DOCKET NUMBER: 212/132
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (213) 489-1600
CC TELEFAX: (213) 955-0440
CC TELETYPE: 67-3510
CC INFORMATION FOR SEQ ID NO: 426:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 27 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC FEATURE:
CC OTHER INFORMATION: The letter "N" stands for the stem II

OTHER INFORMATION: region of a HH ribozyme.
SQ SEQUENCE 27 BP; 10 A; 4 C; 9 G; 0 T; 4 OTHER.

Query Match 40.7%; Score 11; DB 3; Length 27;
Best Local Similarity 66.7%; Pred. No. 1.31e+03;
Matches 16; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

DB 3 CAGACCTGAGCTCAAGTCAGA 26
CP 24 CAGACCTGAGCTCAAGTCAGA 1

RESULT 27
ID PCT-US95-06613-62 STANDARD; DNA; UNC; 29 BP.
AC xxxxxx
DT

DE Sequence 62, Application PC/TUS9506613
CC Sequence 62, Application PC/TUS9506613
CC GENERAL INFORMATION:

CC APPLICANT: STRACKE, MARY; LIOTTA, LANCE;

CC APPLICANT: SCHIFFMANN, ELIOTT; KRUTZSCH,

CC APPLICANT: HENRY, MURATA, JUN

CC TITLE OF INVENTION: MOTILITY STIMULATING

CC TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND

CC NUMBER OF SEQUENCES: 69

CC CORRESPONDENCE ADDRESS:

CC ADDRESSEE: MORGAN & PINNEGAN

CC STREET: 345 PARK AVENUE

CC CITY: NEW YORK

CC STATE: NEW YORK

CC COUNTRY: U.S.A.

CC ZIP: 10154

CC COMPUTER READABLE FORM:

CC MEDIUM TYPE: Floppy disk

CC OPERATING SYSTEM: PC-DOS/MS-DOS

CC SOFTWARE: WordPerfect 5.1

CC CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: PCT/US95/06613

CC FILING DATE: 24-MAY-1995

CC CLASSIFICATION:

CC PRIORITY APPLICATION DATA:

CC APPLICATION NUMBER: 08/346,455

CC FILING DATE: 28-NOV-1994

CC APPLICATION NUMBER DATA:

CC APPLICATION NUMBER: 08/249,182

CC FILING DATE: 25-MAY-1994

CC PRIORITY APPLICATION DATA:

CC APPLICATION NUMBER: 07/822,043

CC FILING DATE: 17-JAN-1992

CC ATTORNEY/AGENT INFORMATION:

CC NAME: DOROTHY R. AUTH

CC REGISTRATION NUMBER: 36,434

CC REFERENCE/DOCKET NUMBER: 2026-41490S2

CC TELECOMMUNICATION INFORMATION:

CC TELEPHONE: (212) 758-4800

CC TELEFAX: (212) 751-6849

CC INFORMATION FOR SEQ ID NO: 62:

CC SEQUENCE CHARACTERISTICS:

CC LENGTH: 29

CC TYPE: nucleic acid

CC STRANDEDNESS: single

CC TOPOLOGY: linear

CC MOLECULE TYPE: CDNA

CC HYPOTHETICAL: NO

CC ANTI-SENSE: NO

CC FEATURE:

CC NAME/KEY:

CC LOCATION:

CC IDENTIFICATION METHOD:

CC OTHER INFORMATION: Nested primer deduced

CC OTHER INFORMATION: from ATX-103, wherein N is inosine

SQ SEQUENCE 29 BP; 3 A; 6 C; 6 G; 4 T; 10 OTHER.

Query Match 40.7%; Score 11; DB 4; Length 29;
Best Local Similarity 35.7%; Pred. No. 1.31e+03;
Matches 5; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

DB 3 YTTGAGATNCARG 16
QY 6 CUUDAGCCUCAGG 19

RESULT 28
ID US-08-476-008-29 STANDARD; DNA; UNC; 31 BP.
AC xxxxxx
DT

DE Sequence 29, Application US/08476008
CC Sequence 29, Application US/08476008
CC Patent No. 5627061

CC GENERAL INFORMATION:

CC APPLICANT: Barry, Gerard F.

CC APPLICANT: Kishore, Ganesh M.

CC APPLICANT: Padgett, Stephen R.

CC APPLICANT: Stallings, William C.

CC TITLE OF INVENTION: Glycosylase Tolerant

CC TITLE OF INVENTION: 5-Ethylpyruvylshikimate-3-Phosphate Synthases

CC NUMBER OF SEQUENCES: 69

CC CORRESPONDENCE ADDRESS:

CC ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. B84F

CC STREET: 700 Chesterfield Village Parkway

CC CITY: St. Louis

CC STATE: Missouri

CC COUNTRY: USA

CC ZIP: 63198

CC COMPUTER READABLE FORM:

CC MEDIUM TYPE: Floppy disk

CC OPERATING SYSTEM: PC-DOS/MS-DOS

CC SOFTWARE: Patent Release #1.0, Version #1.25

CC CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: US/08/476,008

CC FILING DATE: 07-JUN-1995

CC CLASSIFICATION:

CC PRIORITY APPLICATION DATA:

CC APPLICATION NUMBER: 435

CC FILING DATE: 07/576,537

CC CLASSIFICATION: 435

CC ATTORNEY/AGENT INFORMATION:

CC NAME: Hoerner Jr., Dennis R.

CC REGISTRATION NUMBER: 30,914

CC REFERENCE/DOCKET NUMBER: 38-21(10660)A

CC TELECOMMUNICATION INFORMATION:

CC TELEPHONE: (314)537-6047

CC TELEFAX: (314)537-6099

CC INFORMATION FOR SEQ ID NO: 29:

CC SEQUENCE CHARACTERISTICS:

CC LENGTH: 31 base pairs

CC TYPE: nucleic acid

CC STRANDEDNESS: single

CC TOPOLOGY: linear

CC MOLECULE TYPE: Other nucleic acid

CC DESCRIPTION: Synthetic DNA

CC SEQUENCE 31 BP; 2 A; 11 C; 12 G; 6 T; 0 OTHER.

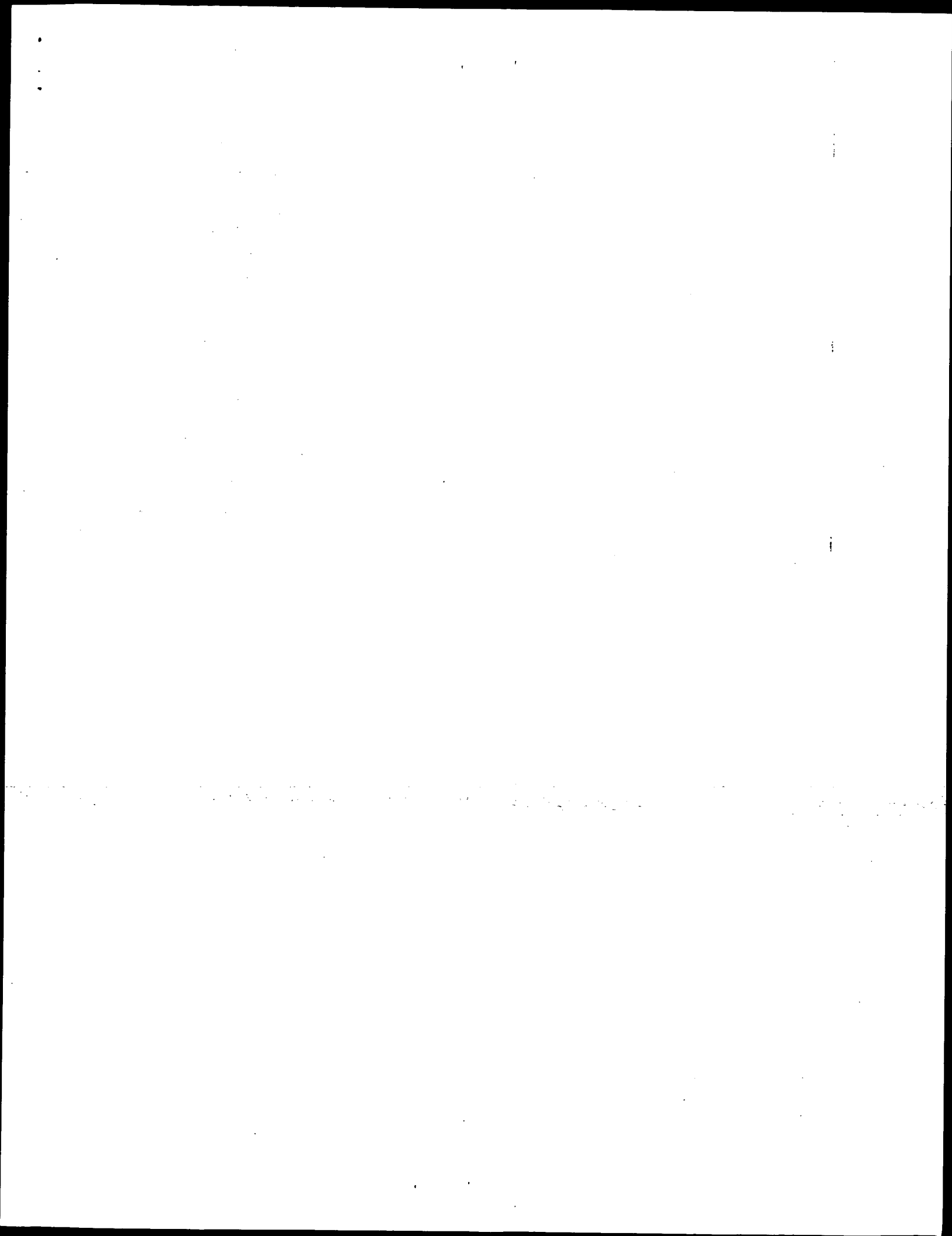
Query Match

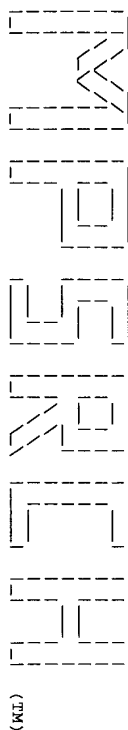
Best Local Similarity 40.7%; Score 11; DB 1; Length 31;
Matches 9; Conservative 4; Mismatches 2; Indels 0; Gaps 0;


```

DE RESULT 30
ID US-08-314-362-7; STANDARD; DNA; UNC; 31 BP.
AC xxxxxx
DT
CC Sequence 7, Application US/08314362
CC Sequence 7, Application US/08314362
CC Patent No. 5532127
CC GENERAL INFORMATION:
CC APPLICANT: Gallatin, W. Michael
CC APPLICANT: Vazeux, Rosemary
CC TITLE OR INVENTION: T-CAM Related Protein
CC NUMBER OF SEQUENCES: 22
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
CC STREET: Two First National Plaza, 20 South Clark
CC STREET: Street
CC CITY: Chicago
CC STATE: Illinois
CC COUNTRY: USA
CC ZIP: 60603
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent In Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/314,362
CC FILING DATE:
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US/07/894,061
CC FILING DATE:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/827,689
CC FILING DATE: 27-JAN-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US
CC FILING DATE: 26-MAY-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: No. 3532127and, Greta E.
CC REGISTRATION NUMBER: 35,302
CC REFERENCE/DOCKET NUMBER: 27866/30918
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (312)346-5750
CC TELEFAX: (312)984-9740
CC TELEX: 25-3856
CC INFORMATION FOR SEQ ID NO: 7:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 31 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: DNA
CC SEQUENCE 31 BP: 7 A; 5 C; 5 G; 6 T; 8 OTHER.
SQ
Query Match 40.7%; Score 11; DB 1; Length 31;
Best Local Similarity 38.5%; Pred. No. 1,31e+03;
Matches 5; Conservative 7; Mismatches 1; Indels 0; Gaps 0;
Db 17 YCTSGCHTBMGS 29
CP 25 TCGACCTGAGC 13

```





 Release 3.1A John F. Collins, Biocomputing Research Unit.
 Copyright (c) 1993-1998 University of Edinburgh, U.K.
 Distribution rights by Oxford Molecular Ltd

Msearch_nu n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Mon Aug 2 11:45:28 1999; MasPar time 107.28 Seconds
 589.719 Million cell updates/sec

Tabular output not generated.

Title: >US-09-121-239-23
 Description: (1-27) from US09121239.seq
 Perfect Score: 27
 N.A. Sequence: 1 UCUGACUUGAGCCUCGAGGUCUGAGU 27
 Comp: AGACTGAACCTCGAGTCCAGACTCA

Scoring table: TABLE default
 Gap 10

Nmitch STD : Dbase 0; Query 0

Searched: 2883791 seqs, 1171580779 bases x 2

Post-processing: Minimum Match 0%
 Listing first 1000 summaries
 Maximum DB seq length 50

Database: emb1-est58
 1:em_est10 2:em_est11 3:em_est17 4:em_est18 5:em_est12
 6:em_est19 7:em_gss1

Database: genbank-est111
 8:gb_est1 9:gb_est10 10:gb_est11 11:gb_est12 12:gb_est13
 13:gb_est14 14:gb_est15 15:gb_est16 16:gb_est17
 17:gb_est18 18:gb_est19 19:gb_est20 20:gb_est21
 21:gb_est22 22:gb_est23 23:gb_est24 24:gb_est25
 25:gb_est26 26:gb_est27 27:gb_est28 28:gb_est29
 29:gb_est30 30:gb_est31 31:gb_est32 32:gb_est33 33:gb_est34
 34:gb_est35 35:gb_est36 36:gb_est37 37:gb_est38 38:gb_est39
 39:gb_gss3 40:gb_gss4 41:gb_gss5 42:gb_gss6

Statistics: Mean 7.131; Variance 1.539; scale 4.632

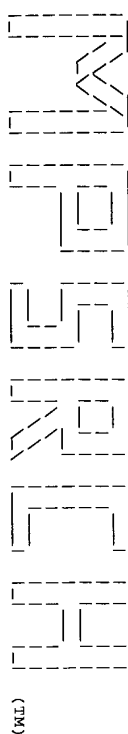
Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	ID	Description	Pred. No.
No matches found.					

Search completed: Mon Aug 2 11:56:07 1999
 Job time : 639 secs.





Release 3.1A John F. Collins, Biocomputing Research Unit.
Copyright (c) 1993-1998 University of Edinburgh, U.K.
Distribution rights by Oxford Molecular Ltd

Msrch_n n.a. - n.a. database search, using Smith-Waterman algorithm
Run on: Mon Aug 2 12:01:16 1999; MasPar time 106.49 Seconds
468.516 Million cell updates/sec
Tabular output not generated.

Title: >US-09-121-239-26
Description: (1-18) from US09121239.seq
Perfect Score: 18
N.A. Sequence: 1 GGAATCATCGAGGCATG 18
Comp: CCTAGTAGCTCCGTACC

Scoring table:
TABLE default
Gap 10

Mnatch STD: Dbase 0; Query 0

Searched: 646147 seqs, 1385953633 bases x 2

Post-processing: Minimum Match 08
Listing first 1000 summaries
Maximum DB seq length 50

Database:

emb158
1:em_ba1 2:em_ba2 3:em_fun 4:em_htg 5:em_hum1 6:em_hum2
7:em_in 8:em_com 9:em_ov 10:em_pat 12:em_ph
13:em_pl 14:em_ro 15:em_sts 16:em_v1
genbank11

Database:
17:gb_ba1 18:gb_ba2 19:gb_htg1 20:gb_htg2 21:gb_in1
22:gb_in2 23:gb_com 24:gb_ov 25:gb_pat 26:gb_ph 27:gb_pl1
28:gb_pl2 29:gb_pr1 30:gb_pr2 31:gb_pr3 32:gb_ro
33:gb_st 34:gb_sts 35:gb_sy 36:gb_un 37:gb_v1

Statistics: Mean 6.224; Variance 2.587; scale 2.406

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	13	72.2	37	25	163515	Sequence 3 from patent 5.66e+02
2	13	72.2	37	25	158617	Sequence 3 from patent 5.66e+02
3	12	66.7	23	25	AR008076	Sequence 2 from patent 2.17e+03

Note: Post-processor removed 997 summaries from list due to search parameters chosen.

ALIGNMENTS

RESULT LOCUS	1	163515	37 bp	DNA	PAT	26-SEP-1997
DEFINITION	Sequence 3 from patent	US 5663070.				

ACCESSION	163515	
NID	g2481088	
VERSION	163515.1	GI:2481088
KEYWORDS		
SOURCE	Unknown.	
ORGANISM	Unknown.	
REFERENCE	Unclassified.	
AUTHORS	1 (bases 1 to 37)	
TITLE	Barri,P.J., Shapiro,J.P. and Kiefer,M.C.	
FEATURES	Recombinant production of a soluble splice variant of the Fas (Apo-1) antigen, fas TM	
SOURCE	Patent: US 5663070-A 3 02-SEP-1997;	
BASE COUNT	1. 37	
ORIGIN	/organism="unknown"	
Query Match	72.2%;	Score 13; DB 25; Length 37;
Best Local Similarity	88.2%;	Pred. No. 5.66e+02;
Matches	15; Conservative	0; Mismatches 2; Indels 0; Gaps 0;

Db	14	GGAATCATCAAGGATG 30
Qy	1	GGAATCATCGAGGCATG 17

RESULT	2	158617	37 bp	DNA	PAT	14-AUG-1997
LOCUS						
DEFINITION	Sequence 3 from patent	US 5652210.				
ACCESSION	158617					
NID	g2477855					
VERSION	158617.1	GI:2477855				
KEYWORDS						
SOURCE	Unknown.					
ORGANISM	Unknown.					

REFERENCE	Unclassified.	
AUTHORS	1 (bases 1 to 37)	
TITLE	Barri,P.J., Shapiro,J.P. and Kiefer,M.C.	
JOURNAL	Soluble splice variant of the Fas (Apo-1) antigen, Fas.DELTA.TM	
FEATURES	Patent: US 5652210-A 3 29-JUL-1997;	
SOURCE	Location/Qualifiers	
BASE COUNT	1. 37	
ORIGIN	/organism="unknown"	

Query Match	72.2%;	Score 13; DB 25; Length 37;
Best Local Similarity	88.2%;	Pred. No. 5.66e+02;
Matches	15; Conservative	0; Mismatches 2; Indels 0; Gaps 0;

Db	14	GGAATCATCAAGGATG 30
Qy	1	GGAATCATCGAGGCATG 17

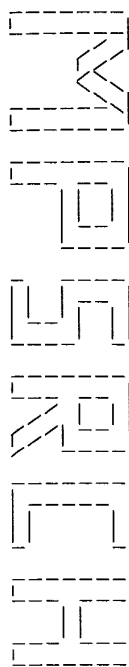
RESULT	3	AR008076	23 bp	DNA	PAT	04-DEC-1998
LOCUS						
DEFINITION	Sequence 2 from patent	US 5753432.				
ACCESSION	AR008076					
NID	93967185					
VERSION	AR008076.1	GI:3967185				
KEYWORDS						
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	Unclassified.					
AUTHORS	1 (bases 1 to 23)					
TITLE	Gudkov,A., Kazarov,A., Mazo,I. and Roninson,I.B.					
JOURNAL	Genes and genetic elements associated with control of neoplastic transformation in mammalian cells					
FEATURES	Patent: US 5753432-A 2 19-MAY-1998;					
SOURCE	Location/Qualifiers					
	1. 23					

BASE COUNT 8 a /organism="unknown"
ORIGIN 7 c 2 g 6 t

Query Match 66.7%; Score 12; DB 25; Length 23;
Best Local Similarity 87.5%; Pred. No. 2,17e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 5 CCATCCATCGATGATT 20
|||||
Cp 18 CCATGCTCGATGATT 3

Search completed: Mon Aug 2 12:09:23 1999
Job time : 487 secs.



(TM)

Release 3.1a John F. Collins, Biocomputing Research Unit.
Copyright (c) 1993-1998 University of Edinburgh, U.K.
Distribution rights by Oxford Molecular Ltd

Mparch_n n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Mon Aug 2 12:15:12 1999; Maspar time 17.94 Seconds

Tabular output not generated. 214,980 Million cell updates/sec

Title: >US-09-121-239-26
Description: (1-18) from US09121239.seq
Perfect Score: 18
N.A. Sequence: 1 GGATCATCGAGCATG 18
Comp: CCTAGTAGCTCCGATAC

Scoring table: TABLE default
Gap 10

Mmatch STD: Dbase 0; Query 0

Searched: 271905 segs, 107135622 bases x 2

Post-processing: Minimum Match 08
Listing first 1000 summaries
Maximum DB seq length 50

Database:

n-gene335
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part32 33:part33
34:part34 35:part35 36:part36 37:part37 38:part38
39:part39 40:part40 41:part41 42:part42 43:part43
44:part44 45:part45 46:part46 47:part47 48:part48
49:part49 50:part50 51:part51 52:part52 53:part53
54:part54 55:part55 56:part56 57:part57 58:part58
59:part59 60:part60

Statistics: Mean 4.989; Variance 2.549; scale 1.957

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	13	72.2	37	15	Q93882 Fas Inton 1 5' PCR P	7.01e+01
2	12	66.7	15	52	V60880 Mutagenic oligonucleo	2.56e+02
3	12	66.7	15	3	O14334 MCP6 603 VH CDR3 walk	2.56e+02
4	12	66.7	20	15	O98678 Adaptor ATG-sense str	2.56e+02
5	12	66.7	23	15	O98679 Adaptor ATG-antisense	2.56e+02
6	12	66.7	23	15	O98679 Adaptor ATG-antisense	2.56e+02
7	12	66.7	27	28	T62501 Proinsulin Ballast Co	2.56e+02
8	12	66.7	30	2	Q11199 Proinsulin Ballast Co	2.56e+02

C	9	11	61.1	21	56	V83708	Probe targeted to the
	10	11	61.1	22	49	V57714	Human chromosome 18 p
	11	11	61.1	23	22	T31558	Ich-3 PCR primer c1CE
	12	11	61.1	23	14	Q79876	Human interleukin-1 b
	13	11	61.1	23	32	T73552	Human interleukin-1 b
	14	11	61.1	23	28	T62502	Murine retrovirus con
	15	11	61.1	27	54	V72603	Peptide nucleic acid
	16	11	61.1	27	28	T62502	Murine retrovirus con
	17	11	61.1	31	50	V67561	Nucleotide fragment c
	18	11	61.1	31	50	V67561	Nucleotide fragment c
	19	11	61.1	37	41	V15733	Primer PINT 316b for
	20	11	61.1	37	18	T03453	Human LAG-3 extracell
	21	11	61.1	37	41	V15732	Primer PINT 316a for
	22	11	61.1	41	51	V51130	Maize polymorphic mar
	23	11	61.1	41	46	V47878	Maize polymorphic sit
	24	10	55.6	19	59	V74222	Cpg-N motif PCR prime
	25	10	55.6	27	60	V99504	T7 promoter/terminato
	26	10	55.6	27	6	Q36213	von Willebrand Factor
	27	10	55.6	48	7	Q46605	Mixed oligonucleotide

Note: Post-processor removed 971 summaries from list due to search parameters chosen.

ALIGNMENTS

RESULT	1
ID	Q93882 standard; cDNA: 37 BP.
AC	Q93882;
DT	06-NOV-1995 (first entry)
DE	Fas Inton 1 5' PCR primer.
KW	Fas-delta-TM; transmembrane deletion; apoptosis; antibody;
KW	adoptive immunotherapy; transgenic animal; primer; PCR;
KW	polymerase chain reaction; ss.
OS	Synthetic.
PN	MO9513701-A.
PD	26-MAY-1995.
PF	15-NOV-1994: U13173.
PR	15-NOV-1993: US-152443.
PA	(LXR-1) LXR BIOTECHNOLOGY INC.
PI	Barr PJ; Kiefer MC; Shapiro JP;
DR	WPI; 95-200120/26.
PT	New nucleic acid encoding Fas protein without its trans-membrane region
PT	- and related vectors, transformed cells, transgenic animals, protein and
PT	antibodies, useful for control of Fas mediated apoptosis
PS	Example 2; Page 14; 38pp; English.
CC	The intron-exon organization of the Fas transmembrane region was
CC	determined by PCR. Primers were designed to flank each of the
CC	putative introns, 1 and 2. The forward and reverse primers
CC	flanking intron 1 are given in Q93882-83, and those for intron 2
CC	in Q93884-85.
CC	Sequence 37 BP; 12 A; 8 C; 8 G; 9 T;
SO	Query Match 72.2%; Score 13; DB 15; Length 37;
SO	Best Local Similarity 88.2%; Pred. No. 7.01e+01;
SO	Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
DB	14 ggaatcatcgagcatg 30
QY	1 GGATCATCGAGCATG 17
RESULT	2
ID	V60880 standard. DNA: 15 BP.
AC	V60880;
DT	25-JUN-1995 (first entry)
DE	Mutagenic oligonucleotide #2 for MAB MCP603 VH CDR3 coding sequence.
KW	Mutagenic oligonucleotides; antigen-binding region; monoclonal antibody;
KW	catalytic site; serine protease; complementarity determining region;
KW	walk-through; ss.
OS	Synthetic.
OS	Homo sapiens.
PN	US5798208-A.
PD	25-AUG-1998.

PF 02-NOV-1992: 930600.
PR 02-NOV-1992: US-930600.
PR 05-APR-1990: US-505314.
PA (CREA/) CREA R.
PI Crea R;
PI WPI: 98-480376/41.
PT Mutagenesis of pre-determined gene sequences - useful for systematic
PT changes of pre-determined amino acids to see their effect on protein
PT activity, and to create gene expression libraries
PS Disclosure: Fig 8E; 33pp; English.
CC The invention relates to a method of generating mutations in proteins by
CC synthesizing a mixture of oligonucleotides in order to alter the codons
CC for specific amino acids within a defined region of the protein. Using a
CC range of oligonucleotides for the mutations, expression libraries of the
CC mutant protein can be constructed. As an example of the method, the
CC antigen-binding region of the monoclonal antibody (MAB) MCP603 (which
CC binds phosphocholine) is altered to contain the catalytic triad residues
CC for a serine protease. Specifically the amino acids to be altered are
CC selected from the Asp of the complementarity determining region (CDR) 1
CC region of the variable heavy chain (VH) of the antibody, the His of VH
CC CDR3 and the Ser of the CDR2 from the light chain variable region (VL).
CC The mutagenesis is by a "walk-through" method. The sequence presented
CC here corresponds to the degenerate mutagenic oligonucleotide used to
CC construct an expression library encoding novel CDR3 sequences from the
CC Vh region of the MAB (see V60862).
SQ Sequence 15 BP; 0 A; 3 C; 0 G; 2 T;

Query Match 66.7%; Score 12; DB 52; Length 15;
Best Local Similarity 35.7%; Pred. No. 2.56e+02;
Matches 5; Conservative 8; Mismatches 1; Indels 0; Gaps 0;

Db 2 rcbmcmtvtrbmc 15
Cp 14 GCCTGCATGATTC 1

RESULT 3
ID 014334 standard; DNA; 15 BP.

AC 014334:
DT 15-JAN-1992 (first entry)
DE MCP6 603 VH CDR3 walk-through mutagenesis oligonucleotide (DHS).
KW Mutagenesis; monoclonal antibody; Fv molecule; ss.
OS Synthetic.
PN MO9115581-A.
PD 17-OCT-1991.
PF 05-APR-1991: U02362.
PR 05-APR-1990: US-505314.
PA (CREA/) CREA R.
PI Crea R;
PI WPI: 91-325224/44.
PT Walk-through mutagenesis of proteins - by introducing predetermined
PT amino acid in each sequence position in preselected region of the
PT protein.
PS Disclosure: Fig 8E; 91pp; English.
CC Walk-through mutagenesis of five out of six CDRs of the MCP6 603 Fv
CC molecule is performed, and Asp, His and Ser are the preselected amino
CC acids. In this model, walk-through mutagenesis is carried out from two
CC to three times with a different amino acid in a given region or domain.
CC E.g., Ser and His are sequentially walked-through VL CDR1 (014330),
CC and Asp and Ser are sequentially walked-through VL CDR3 (014331).
CC VL CDR2 was not targeted for mutagenesis because structural studies
CC indicated that this region contributes little to the binding site in
CC MCP6 603. In CDR1 of the VH chain of the Fv, Asp and His are walked
CC through (014332). Ser can be introduced at two positions in CDR1
CC with a single base change. In VH CDR2, His and Ser are the
CC preselected amino acids used (014333) and in VH CDR3, Asp, His
CC and Ser are each walked through the amino terminal five positions
CC of CDR3.
CC See also 014321-34.
SQ Sequence 15 BP; 0 A; 3 C; 0 G; 2 T;

Query Match 66.7%; Score 12; DB 3; Length 15;
Best Local Similarity 35.7%; Pred. No. 2.56e+02;

Matches 5; Conservative 8; Mismatches 1; Indels 0; Gaps 0;
Db 2 rcbmcmtvtrbmc 15
Cp 14 GCCTGCATGATTC 1

RESULT 4
ID 098678 standard; DNA; 20 BP.

AC 098678:
DT 20-DEC-1995 (first entry)
DE Adaptor ATG-sense strand.
KW Genetic suppressor element; Tr6-GSE; fibroblast; transformation;
KW retrovirus; tumor; cancer; gene therapy; adaptor; ss.
OS Synthetic.
PN MO9523855-A2.
PD 08-SEP-1995.
PF 01-MAR-1995: U02521.
PR 02-MAR-1994: US-204740.
PA (UNIT) UNIV ILLINOIS FOUND.
PI Gudkov A, Kazarov A, Mazo I, Roninson IB;
PI WPI: 95-320570/41.
PT Isolation of genetic suppressor elements (GSEs) - useful in
PT diagnostic assays for determining GSE mRNA expression levels and in
PT the treatment of malignant cancers
PS Example 1; Fig.1; 61pp; English.
CC Poly-A+ RNA fragments obtd. from mouse fibroblast NIH3T3 cells were
CC used to prepare double-stranded cDNA. This was then ligated to an
CC adaptor that provided ATG codons in all 3 reading frames, and was
CC used to prepare a normalized random fragment cDNA library.
SQ Sequence 20 BP; 6 A; 2 C; 7 G; 5 T;

Query Match 66.7%; Score 12; DB 15; Length 20;
Best Local Similarity 87.5%; Pred. No. 2.56e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 1 aatcatcgatgatgg 16
Cp 3 AATCATCGAGCATGG 18

RESULT 5

ID 098679 standard; DNA; 23 BP.
AC 098679:
DT 20-DEC-1995 (first entry)
DE Adaptor ATG-antisense strand.
KW Genetic suppressor element; Tr6-GSE; fibroblast; transformation;
KW retrovirus; tumor; cancer; gene therapy; adaptor; ss.
OS Synthetic.
PN MO9523855-A2.
PD 08-SEP-1995.
PF 01-MAR-1995: U02521.
PR 02-MAR-1994: US-204740.
PA (UNIT) UNIV ILLINOIS FOUND.
PI Gudkov A, Kazarov A, Mazo I, Roninson IB;
PI WPI: 95-320570/41.
PT Isolation of genetic suppressor elements (GSEs) - useful in
PT diagnostic assays for determining GSE mRNA expression levels and in
PT the treatment of malignant cancers
PS Example 1; Fig.1; 61pp; English.
CC Poly-A+ RNA fragments obtd. from mouse fibroblast NIH3T3 cells were
CC used to prepare double-stranded cDNA. This was then ligated to an
CC adaptor that provided ATG codons in all 3 reading frames, and was
CC used to prepare a normalized random fragment cDNA library.
SQ Sequence 23 BP; 8 A; 7 C; 2 G; 6 T;

Query Match 66.7%; Score 12; DB 15; Length 23;
Best Local Similarity 87.5%; Pred. No. 2.56e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 5 ccacatcgatgatatt 20
Cp 18 CCATGCCTGCATGATT 3


```
RESULT 6
ID Q1198 standard; DNA: 24 BP.
AC Q1198:
DE 05-JUN-1991 (first entry)
DE Proinsulin Ballast Constituent-coding sequence #1.
KW Ballast constituent; fusion protein; oligonucleotide library;
KW proinsulin; ss.
OS Synthetic.
FH Key
FT repeat_unit
FT 7..9
FT /tag= a
FT /note= "can be present 3 to 6 times"
PN W09103550-A.
PD 21-MAR-1991.
PF 28-AUG-1990; U04840.
PR 29-AUG-1989; US-399874.
PA (FARH ) HOECHST AG.
PA (GEMO-) GEN HOSPITAL CORP.
PI Stengel S, Ulmer W, Habermann P, Uhlmann E, Seed B;
PI WPI: 91-102070/14.
PT Prep. of fusion proteins contg. ballast constituent and protein
PT - giving prods. which are protease resistant or insoluble
PS Claim 13: Page 51: 60pp: English.
CC This oligonucleotide is an example of a member of an oligonucleotide
CC library encoding ballast constituents. The oligonucleotides are
CC inserted into a vector, functionally linked to a regulatory region
CC and to the proinsulin structural gene. Host cells transformed with
CC such plasmids produce proinsulin ballast fusion proteins in
CC high yield. The ballast is short and does not disturb the folding of
CC the proinsulin. The fusion protein is soluble or easily
CC solubilised. The oligonucleotide encodes a cleavage site at its 3'
CC end which allows easy removal of the ballast constituent.
CC See also Q1194-7 and Q1199-Q1202.
SQ Sequence 24 BP; 2 A; 6 C; 5 G; 1 T;

Query Match 66.7%; Score 12; DB 2; Length 24;
Best Local Similarity 42.9%; Pred. No. 2.56e+02;
Matches 6; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

DB 9 dddcdcdcdagc 22
QY 1 GGATCATCGAGC 14

RESULT 7
ID T62501 standard; DNA: 27 BP.
AC T62501:
DE 28-APR-1997 (first entry)
DE Murine retrovirus consensus left side integration response sequence.
KW Consensus sequence; left side; integration response; LTR.
KW Long terminal repeat; retroviral attachment sequence; preparation;
KW gene delivery construct; ss.
OS Murine retrovirus.
PD 06-SEP-1996.
PF 28-FEB-1996; U02877.
PR 28-FEB-1995; US-395355.
PA (UYCR-) UNIV CREIGHTON.
PA Hodgson CP;
DR WPI: 96-412589/41.
PT Gene delivery system including liposome or dendrimer and
PT penetration molecule - esp. for gene therapy, provides efficient
PT and stable expression of chimeric genes more safely than use of
PT viruses.
PS Example 3: Fig 2: 50pp: English.
CC The present sequence is the murine retrovirus consensus left side
CC (UT) integration response sequence, which reads into the long
CC terminal repeat (LTR). It can be used as a retroviral attachment
CC sequence in the preparation of a gene delivery construct.
SQ Sequence 27 BP; 4 A; 0 C; 1 G; 1 T;
```

```
Query Match 66.7%; Score 12; DB 28; Length 27;
Best Local Similarity 0.0%; Pred. No. 2.56e+02;
Matches 0; Conservative 13; Mismatches 4; Indels 0; Gaps 0;

DB 7 rrwbyhrvhdhndk 23
QY 2 GGATCATCGAGC 18

RESULT 8
ID Q1199 standard; DNA: 30 BP.
AC Q1199:
DE 05-JUN-1991 (first entry)
DE Proinsulin Ballast Constituent-coding sequence #2.
KW Ballast constituent; fusion protein; oligonucleotide library;
KW proinsulin; ss.
OS Synthetic.
FH Key
FT repeat_unit
FT 7..9
FT /tag= a
FT /note= "may be present 3 to 6 times"
PN W09103550-A.
PD 21-MAR-1991.
PF 28-AUG-1990; U04840.
PR 29-AUG-1989; US-399874.
PA (FARH ) HOECHST AG.
PA (GEMO-) GEN HOSPITAL CORP.
PI Stengel S, Ulmer W, Habermann P, Uhlmann E, Seed B;
PI WPI: 91-102070/14.
PT Prep. of fusion proteins contg. ballast constituent and protein
PT - giving prods. which are protease resistant or insoluble
PS Claim 13: Page 51: 60pp: English.
CC This oligonucleotide is an example of a member of an oligonucleotide
CC library encoding ballast constituents. The oligonucleotides are
CC inserted into a vector, functionally linked to a regulatory region
CC and to the proinsulin structural gene. Host cells transformed with
CC such plasmids produce proinsulin ballast fusion proteins in
CC high yield. The ballast is short and does not disturb the folding of
CC the proinsulin. The fusion protein is soluble or easily
CC solubilised. The oligonucleotide encodes a cleavage site at its 3'
CC end which allows easy removal of the ballast constituent.
CC See also Q1194-8 and Q1200-Q1202.
SQ Sequence 30 BP; 2 A; 8 C; 6 G; 1 T;

Query Match 66.7%; Score 12; DB 2; Length 30;
Best Local Similarity 42.9%; Pred. No. 2.56e+02;
Matches 6; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

DB 15 dddcdcdcdagc 28
QY 1 GGATCATCGAGC 14

RESULT 9
ID V83708 standard; DNA: 21 BP.
AC V83708:
DE 26-FEB-1999 (first entry)
DE Probe targeted to the 3.8S rDNA gene.
KW Internal transcribed spacer 2; ITS2; probe; Aspergillus flavus;
KW A. niger; A. terreus; A. nidulans; Fusarium solani; F. moniliforme;
KW Mucor rouxii; W. racemosus; W. plumbeus; R. indicus; A. fumigatus;
KW R. circinellus; F. circinellus; Rhizopus oryzae; R. microsporus;
KW Cunninghamella elegans; Pseudallesheria boydii; Scedosporium apiospermum;
KW Penicillium notatum; Sporothrix schenckii; filamentous fungus; ss.
OS Synthetic.
FH Key
FT modified_base 1
FT /tag= a
FT /note= "labelled with biotin"
PN W09850584-A2.
PD 12-NOV-1998.
PF 01-MAY-1998; U08926.
```

PR 02-MAY-1997; US-045400.
 PA (US\$H) US DEPT HEALTH & HUMAN SERVICES.
 PI Aidorevich L, Choi JS, Morrison CJ, Reiss E;
 PR WPI, 99-034737/03.
 PT New nucleic acid probes for filamentous fungi - for detecting e.g.
 PT Aspergillus, Fusarium, Mucor, Rhizopus, Rhizomucor, Absidia,
 PT Cunninghamella, Pseudallescheria boydii, Penicillium and Sporothrix
 PT species.
 PS Claim 48; Page 22; 45pp; English.
 CC Probes V83677-708 are derived from the internal transcribed spacer 2
 CC (ITS2) region of various filamentous fungi (see V70845-73). The probes
 CC are species-specific, and can be used for identifying a species selected
 CC from Aspergillus flavus, A. fumigatus, A. niger, A. terreus, A. nidulans,
 CC Fusarium solani, F. moniliforme, Mucor rouxii, M. raeticus, M. plumbeus,
 CC M. indicus, M. circinaloides I, Circinaloides, Rhizopus oryzae,
 CC R. microsporus, R. circinans, R. stolonifer, Rhizomucor pusillus,
 CC Absidia corymbifera, Cunninghamella elegans, Pseudallescheria boydii
 CC (teleomorph of Scedosporium apiospermum), Penicillium notatum, or
 CC Sporothrix schenckii. The probes can be used for differentiating
 CC filamentous fungal species from each other and from other medically
 CC important fungi.
 SQ Sequence 21 BP; 6 A; 4 C; 4 G; 6 T;

Db 1 gaatcatgag 11
 |||||||||
 Qy 2 GAATCATGAG 12

RESULT 10
 ID V57714 standard; DNA; 22 BP.
 AC V57714;
 DF 18-NOV-1998 (first entry)
 DE Human chromosome 18 PCR mapping primer clone 7r.
 KW Manic-depressive illness; susceptibility; genotype; diagnosis;
 KW chromosomal marker; polymorphic marker; chromosome 18; human;
 KW myo-inositol monophosphatase protein; IMP-18p; PCR primer; ss.
 OS Synthetic.
 OS Homo sapiens.
 PN M09818963-A1.
 PF 07-MAY-1998.
 PD 28-OCT-1997; U19381.
 PR 28-OCT-1996; US-029278.
 PA (US\$H) US DEPT HEALTH & HUMAN SERVICES.
 PI Badner JV, Berrettini WH, Detera-Wadleigh SD, Esterling LE,
 PI Gershon ES, Goldin LR, Sanders AR, Yoshikawa T;
 DR WPI, 98-272247/24.
 PT New isolated IMP-18p myo-inositol monophosphatase - used to develop
 PT products for determining susceptibility to manic depressive illness
 PT and as targets for preventive and therapeutic treatments
 PS Example 5; Page 71; 118pp; English.
 CC A method has been developed for determining a genotype associated with
 CC increased susceptibility to manic-depressive (MD) illness. The method
 CC comprises determining the genotype of an affected individual with at
 CC least one polymorphic marker localised within the chromosomal region
 CC defined by and including markers D18S843 and D18S869 and determining the
 CC genotype associated with increased susceptibility to MD disorder. The
 CC method can be used for determining susceptibility to MD illness
 CC including bipolar disorder, genetic counselling of individuals from
 CC families affected with MD illness, and aid in the differential diagnosis
 CC of MD illness from other psychiatric pathologies. Products from the
 CC present invention can also be used to obtain modulators of IMP-18p myo-
 CC inositol monophosphatase protein activity and as targets for preventive
 CC and therapeutic treatments. The present sequence represents a PCR primer
 CC used in the mapping of human chromosome 18 for determining the genotype
 CC of MD illness susceptibility, used in an example from the present
 CC invention. 22 BP; 7 A; 3 C; 6 G; 6 T;

Query Match 61.1%; Score 11; DB 56; Length 21;
 Best Local Similarity 90.9%; Pred. No. 8.84e-02;
 Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Best Local Similarity 100.0%;	Pred. No. 8,94e+02;
Matches 11; Conservative 0;	Mismatches 0; Indels 0; Gaps 0;
<p>Db 7 gctcgcagtcgat 17 </p>	
Cp 14 GCCTCGAGTCAT 4	
<p>RESULT 11 ID T31558 standard; DNA; 23 BP. AC T31558; DT 25-SEP-1996 (first entry) DE Ich-3 PCR primer c1CEAs. KW Ich-3; ICB-ced-3 homologue; programmed cell death; apoptosis; KW Interleukin-1 beta converting enzyme; gene therapy; primer; PCR; KW polymerase chain reaction; ss. OS Synthetic. PN WO9620721-A1. PD 11-JUL-1996. PF 04-JAN-1996; U00177. PR 04-JAN-1995; US-368704. PA (GEHO) GEN HOSPITAL CORP. PI Miura M, Yuan J; PI WPI: 96-333763/73. PT Preventing or promoting programmed cell death in vertebrate cells PT comprises inhibiting or increasing the activity of PT interleukin-1-beta converting enzyme, or altering expression of PT other related genes PS Disclosure; Page 24, 127pp; English. CC PCR primers c1CEB (T31557) and c1CEAs (T31556) were used to CC amplify cDNA from embryonic day 14 mouse brain cDNA. cDNA CC (T31554) coding for a novel homologue, Ich-3 (R98464), of CC interleukin-1 beta converting enzyme was isolated. This can CC be used in methods of controlling programmed cell death. CC Sequence 23 BP; 5 A; 5 C; 6 G; 4 T;</p>	
<p>Query Match 61.1%; Score 11; DB 22; Length 23; Best Local Similarity 78.6%; Pred. No. 8.84e+02; Matches 11; Conservative 1; Mismatches 2; Indels 0; Gaps 0;</p>	
<p>Db 4 athatcagcgcgt 17 : </p>	
Cy 4 ATCATCGAGTCAT 17	
<p>RESULT 12 ID Q79976 standard; DNA; 23 BP. AC Q79976; DT 13-SEP-1995 (first entry) DE Human interleukin-1 beta converting enzyme Ice-4 PCR primer c1CEAs. KW Human interleukin-1 beta converting enzyme homolg; Ice-4; KW oncogene bcl-2; programmed cell death; cancer treatment; KW PCR primer c1CEAs; ss. OS Synthetic. PN WO9500160-A. PD 05-JAN-1995. PF 10-JUN-1994; U06630. PR 24-JUN-1993; US-080850. PA (GEHO) GEN HOSPITAL CORP. PI Miura M, Yuan J; PI WPI: 95-051742/17. PT Promoting or preventing programmed cell death in vertebrate cells PT - by inhibiting the activity of Interleukin-1 beta converting PT enzyme. PS Disclosure; Page 22; 116pp; English. CC Q79975 and Q79976 are a pair of primers for the PCR amplification CC of Q79966, which encodes R56769 human interleukin-1 beta converting CC enzyme homolg (Ice-4), increasing Ice-4s enzymatic activity can CC promote the programmed cell death of cancer cells (pref. those CC overexpressing the bcl-2 oncogene), this can be used as the basis CC of a new cancer treatment. Alternatively by reducing Ice-4s enzymatic CC activity programmed cell death can be inhibited, this may be useful CC in the development of new cell lines which remain viable in culture</p>	

SC for extended or indefinite periods, independent of growth factors.
 Sequence 23 BP; 5 A; 5 C; 6 G; 4 T;
 Query Match 61.1%; Score 11; DB 14; Length 23;
 Best Local Similarity 78.6%; Pred. No. 8.84e+02;
 Matches 11; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 4 ataccagcagctg 17
 11:|||||111111
 4 ATCATCATCAGCAGC 17

QY

RESULT 13
 ID T75952 standard; DNA; 25 BP.
 AC T75952;
 DT 15-SEP-1997 (first entry)
 DE DEN-2 cloning/sequencing sense primer, D2-2702.
 KW Dengue 2 virus; polyprotein; capsid; prM; M; E; NS1; NS2A; NS2B; NS3;
 KW NS4A; NS4B; NS5; PDK-53; quadravalent vaccine; immunity; serotype;
 KW chimeric DEN-2/1 virus; chimeric DEN-2/3 virus; chimeric DEN-2/4 virus;
 KW dengue fever; fatal dengue haemorrhagic fever; dengue shock syndrome;
 KW DHF; DSS; PCR; amplify; polymerase chain reaction; primer; ss.
 OS Synthetic.
 PN MO9640933-A1.
 PD 19-DEC-1996.
 PR 06-JUN-1996; U09209.
 PA (UYMA-) UNIV MAHIDOL AT SALAYA.
 PA (USSR-) US DEPT HEALTH & HUMAN SERVICES.
 PI Bhamraprati N, Butrapet S, Chang J, Gubler DJ;
 PI Halstead SB, Kinney K, Trent DW;
 PI WPI: 97-05330/05.
 PT PDK-53, a clone of infectious attenuated Dengue 2 virus strain 16681
 PT - also chimeric DEN-2/1, DEN-2/3 and DEN-1/4 viruses; used as a
 PT quadravalent vaccine for protecting against Dengue virus infection
 PS Examples: Page 101; 261pp; English.
 CC The sequences given in T75909-T76029 are primers which were used in
 CC the amplification, cloning and sequencing of the Dengue 2 viral cDNA's
 CC of the invention. The Dengue 2 viral DNA encodes a polyprotein which
 CC comprises the capsid, prM, M, E, NS1, NS2A, NS2B, NS3, NS4A, NS4B and
 CC NS5 proteins. The quadravalent vaccine of the invention comprises an
 CC attenuated Dengue virus clone, PDK-53, and a chimeric DEN-2/1 virus.
 CC a chimeric DEN-2/3 virus, and/or a chimeric DEN-2/4 virus. The new
 CC quadravalent vaccines are used to protect against infection by all
 CC four serotypes of dengue virus, DEN-1, DEN-2, DEN-3 and DEN-4, which
 CC can lead to dengue fever or fatal dengue haemorrhagic fever/dengue
 CC shock syndrome (DHF/DSS). Host cells are used to produce the recombinant
 CC protein products of the DNA constructs which are used in the
 CC vaccines.
 CC Sequence 25 BP; 11 A; 4 C; 8 G; 2 T;

QY

Query Match 61.1%; Score 11; DB 32; Length 25;
 Best Local Similarity 86.7%; Pred. No. 8.84e+02;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 3 ggaatcatgcagcga 17
 11:|||||111111
 1 GGATCATCATCAGCAGCA 15

QY

RESULT 14
 ID T62502 standard; DNA; 27 BP.
 AC T62502;
 DT 28-APR-1997 (first entry)
 DE Murine retrovirus consensus right side integration response sequence.
 KW Consensus sequence; right side; integration response; LTR;
 KW long terminal repeat; retroviral attachment sequence; preparation;
 KW gene delivery construct; ss.
 OS Murine retrovirus.
 PN MO9626745-A1.
 PD 06-SEP-1996.
 PR 28-FEB-1996; U02877.
 PR 28-FEB-1995; US-395355.

PA (UYCR-) UNIV CRISTIGHTON.
 PI Hodgson CP;
 DR WPI: 96-412589/41.
 PT Gene delivery system including liposome or dendrimer and
 PT perpetuation molecule - esp. for gene therapy, provides efficient
 PT and stable expression of chimeric genes more safely than use of
 PT viruses.
 PS Example 3; Fig 2; 50pp; English.
 CC The present sequence is the murine retrovirus consensus right side
 CC (U5) integration response sequence, which reads towards the outside
 CC of the long terminal repeat (LTR). It can be used as a retroviral
 CC attachment sequence in the preparation of a gene delivery construct.
 CC Sequence 27 BP; 1 A; 2 C; 0 G; 6 T;

QY

Query Match 61.1%; Score 11; DB 28; Length 27;
 Best Local Similarity 0.0%; Pred. No. 8.84e+02;
 Matches 0; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

Db 6 sbshbhyvrrt 18
 :::::::::::::::
 1 GGATCATCATCAGG 13

QY

RESULT 15
 ID V72603 standard; DNA; 27 BP.
 AC V72603;
 DT 11-FEB-1999 (first entry)
 DE Peptide nucleic acid molecule #3.
 KW peptide nucleic acid; PNA; 2-dimensional; 3-dimensional; nanometer;
 KW geometric structure; supramolecular; computer chip; conductive;
 KW insulator; robot arm; network; ss.
 OS Synthetic.
 PN Key
 FH modified_base 1 Location/Qualifiers
 FT FT
 FT FT
 FT FT
 FT modified_base 27 /note= "attached to a hydrogen group"
 FT FT
 FT FT
 FT modified_base 27 /note= "attached to an amide group"
 FT FT
 FT BP-881228-N2.
 PD 02-DEC-1998.
 PD 26-MAY-1998; 109492.
 PR 30-MAY-1997; EP-108670.
 PA (BOEF) BOEHRINGER MANNHEIM GMBH.
 PI Batz H, Hansen HF, Koch T;
 PI WPI: 99-001349/01.
 DR Useful for preparation of fine networks in nanometer size.
 PT Constructing defined oligo- or polymeric geometric structure -
 PS Example 2; Page 9; 12pp; English.
 CC The present invention describes a method for constructing a defined
 CC oligo- or polymeric geometric structure. The method comprises combining
 CC a first oligomeric element having bound recognition elements with a
 CC second oligomeric element having bound recognition elements capable of
 CC recognising the recognition elements of the first unit under binding
 CC conditions. The recognition elements are heterocyclic moieties
 CC recognising other elements by hydrogen bonding, van-der-Waals
 CC interaction, pi-stacking or water exclusion (the recognition elements
 CC of at least one oligomeric element are bound to space defined locations
 CC of a nucleic acid analogue). The geometric structures are useful for the
 CC preparation of fine networks, robot arms of nanometer scale and new
 CC networks of computer chips.
 CC materials and polymers with conductivity and/or insulator properties.
 CC The present sequence represents a peptide nucleic acid molecule used in
 CC an example from the present invention for the assembly of a double fork
 CC geometric structure containing 6 nucleic acid analogues.
 CC Sequence 27 BP; 7 A; 6 C; 8 G; 6 T;

QY

Query Match 61.1%; Score 11; DB 54; Length 27;
 Best Local Similarity 82.4%; Pred. No. 8.84e+02;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 9 gtagcatgcagcagc 25
 11:|||||111111

QY 1 GGAATCATCGAGCATG 17

RESULT 16

ID T62502 standard; DNA; 27 BP.
AC T62502;
DE 28-APR-1997 (first entry)
DE Murine retrovirus consensus right side integration response sequence.
DE Consensus sequence; right side; integration response; LTR;
KW long terminal repeat; retroviral attachment sequence; preparation;
KW gene delivery construct; ss.
OS Murine retrovirus.
PN M09626745-A1.
PD 06-SEP-1996.
PF 28-FEB-1996; 002877.
PR 28-FEB-1995; US-395355.
PA (UYCR-) UNIV CREIGHTON.
PI Hodgson CP;
DR WPI: 96-412589/41.
PT Gene delivery system including liposome or dendrimer and
PT percutaneous molecule - esp. for gene therapy, provides efficient
PT and stable expression of chimeric genes more safely than use of
PT viruses.
PS Example 3; Fig 2; 50pp; English.
CC The present sequence is the murine retrovirus consensus right side
CC (U5) integration response sequence, which reads towards the outside
CC of the long terminal repeat (LTR). It can be used as a retroviral
CC attachment sequence in the preparation of a gene delivery construct.
SQ Sequence 27 BP; 1 A; 2 C; 0 G; 6 T;

Query Match

Best Local Similarity 61.1%; Score 11; DB 28; Length 27;
Matches 0; Conservative 11; Mismatches 0; Indels 0; Gaps 0;

Db 7 bshbhyvyr 17

Cp 18 CCATGCTCGA 8

RESULT 17

ID V67561 standard; DNA; 31 BP.
AC V67561;
DE 21-DEC-1998 (first entry)
DE Nucleotide fragment containing polymorphic site, WI-15260.
KW ss: polymorphic site; nucleic acid analysis; diagnosis; monitoring;
KW cancer; inflammation; heart disease; CNS disease.
OS Homo sapiens.
PN W09838846-A2.
PD 11-SEP-1998.
PF 06-MAR-1998; U04571.
PR 28-MAR-1997; US-042125.
PR 07-MAR-1997; US-813159.
PA (AFY-) AFFYMETRIX INC.
PI Berno A, Chee M, Fan J, Lipshutz RJ;
DR WPI: 96-495419/42.
PT New nucleic acid segments containing polymorphic sites, or
PT complements and methods of detecting a nucleic acid - for general
PT use including diagnosis and monitoring of diseases
PS Claim 1; Page 15; 42pp; English.
CC New nucleic acid segment comprising one of the 10 - 100 bp sequences
CC given in the specification (sequences of a polymorphic site), or the
CC complement of the segment and a method of analysing a nucleic acid
CC comprising determining the base occupying the polymorphic site of the
CC polymorphic fragment sequences are disclosed in the specification. The
CC information obtained from nucleic acid analysis by the method described
CC is useful in diagnosis or monitoring of diseases like cancer,
CC inflammation, heart disease, CNS diseases, and susceptibility to
CC infection by microorganisms. In addition, the nucleic acid segments are
CC useful in manufacturing medication in the treatment of prophylaxis of
CC diseases, and also the use of the DNA segments as pharmaceutical.
SQ Sequence 31 BP; 9 A; 7 C; 9 G; 5 T;

Query Match

61.1%; Score 11; DB 50; Length 31;

Best Local Similarity 84.6%; Pred. No. 8.84e+02;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 7 aatcatcgagca 19

QY 3 AATCATCGAGCA 15

RESULT 18

ID V67733 standard; DNA; 31 BP.
AC V67733;
DE 24-DEC-1998 (first entry)
DE Nucleotide fragment containing polymorphic site, WI-5835.
DE ss: polymorphic site; nucleic acid analysis; diagnosis; monitoring;
KW cancer; inflammation; heart disease; CNS disease.
OS Homo sapiens.
PN M09838846-A2.
PD 11-SEP-1998.
PF 06-MAR-1998; U04571.
PR 28-MAR-1997; US-042125.
PR 07-MAR-1997; US-813159.
PA (AFY-) AFFYMETRIX INC.
PI Berno A, Chee M, Fan J, Lipshutz RJ;
DR WPI: 96-495419/42.
PT New nucleic acid segments containing polymorphic sites, or
PT complements and methods of detecting a nucleic acid - for general
PT use including diagnosis and monitoring of diseases
PS Claim 1; Page 21; 42pp; English.
CC New nucleic acid segment comprising one of the 10 - 100 bp sequences
CC given in the specification (sequences of a polymorphic site), or the
CC complement of the segment and a method of analysing a nucleic acid
CC comprising determining the base occupying the polymorphic site of the
CC polymorphic fragment sequences are disclosed in the specification. The
CC information obtained from nucleic acid analysis by the method described
CC is useful in diagnosis or monitoring of diseases like cancer,
CC inflammation, heart disease, CNS diseases, and susceptibility to
CC infection by microorganisms. In addition, the nucleic acid segments are
CC useful in manufacturing medication in the treatment of prophylaxis of
CC diseases, and also the use of the DNA segments as pharmaceutical.
SQ Sequence 31 BP; 12 A; 4 C; 3 G; 11 T;

Query Match

Best Local Similarity 76.5%; Score 11; DB 50; Length 31;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Db 2 aatcatcgagca 18

Cp 17 CATGCTCGAGTCC 1

RESULT 19

ID V15733 standard; DNA; 37 BP.
AC V15733;
DE 26-JUN-1998 (first entry)
DE Primer PINT 316b for insulin analogue preparation.
DE Insulin analogue; histidine-rich B-chain domain; treatment;
KW diabetes; zinc-binding; delayed release; PCR primer;
KW subcutaneous administration; ss.
OS Synthetic.
PN Homo sapiens.
PD EP-821006-A2.
PN 28-JAN-1998.
PF 17-JUL-1997; 112197.
PR 26-JUL-1996; DE-030242.
PA (FARR) HOECHST AG.
PI Ertl J, Geisen K, Habermann P, Seipke G;
DR WPI: 96-102618/10.
PT Insulin analogues with histidine-rich B-chain domain - with high
PT zinc-complexing capacity, useful for treatment of diabetes
PS Example 3; Page 7; 22pp; German.
CC The present sequence was used in the preparation of insulin
CC analogues with histidine-rich B-chain domain, which can be used in
CC pharmaceutical formulations for treating diabetes. The analogues

CC have a greater zinc-binding capacity than conventional forms of
 CC insulin, forming stable complexes having delayed release properties
 CC on subcutaneous administration; 8 A; 13 C; 12 G; 4 T;
 SQ Sequence 37 BP; 8 A; 13 C; 12 G; 4 T;
 Query Match 61.1%; Score 11; DB 41; Length 37;
 Best Local Similarity 92.3%; Pred. No. 8.84e+02;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Db 18 atccatcgagcat 30
 4 ATCATCGAGCAT 16
 QY
 RESULT 20
 ID T03453 standard; DNA; 37 BP.
 AC T03453;
 DT 14-JUN-1996 (first entry)
 DE Human IAG-3 extracellular domain D1 amplification primer.
 KW Immunoglobulin extracellular domain; Ig superfamily; membrane protein;
 KW soluble; IAG-3; immunosuppression; MHC class II; binding; target;
 KW Natural killer; NK cell; activated T lymphocyte; CD4-related; ss.
 OS Synthetic.
 PN WO9530750-A2.
 PD 16-NOV-1995.
 PR 06-MAY-1994; FR-005643.
 PA (ISTE) ARS APPLIED RES SYST HOLDING NV.
 PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
 PA (INSR) INST ROUSSY GUSTAVE.
 PI Faure F, Herceud T, Huard B, Triebel F;
 DR WPI; 95-404117/51.
 PT New soluble polypeptide contg. extracellular domains of IAG-3 -
 PT useful as immunosuppressant and to generate antibodies for use as
 PT immunostimulants
 Example 3; Page 18; 69pp; French.
 CC Soluble polypeptides comprising at least part of one of the four
 CC Ig-like extracellular domains of IAG-3 (see R87089) are claimed.
 CC The sol. polypeptides bind to MHC class II molecules, making them
 CC useful as immunosuppressants or, when coupled to a toxin or radio-
 CC isotope, for targeted destruction of cells which express MHC class
 CC II molecules (e.g. leukemia or melanoma cells). Antibodies to the
 CC polypeptides act as immunostimulants. The present sequence is that
 CC of a PCR primer used for amplifying DNA coding for domain D1
 CC of IAG-3 for inclusion in an expression vector. 5 T;
 CC Sequence 37 BP; 6 A; 13 C; 13 G;
 SQ
 Query Match 61.1%; Score 11; DB 18; Length 37;
 Best Local Similarity 92.3%; Pred. No. 8.84e+02;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Db 14 catcgagcctg 26
 6 CATCGAGCATG 18
 QY
 RESULT 21
 ID V15732 standard; DNA; 37 BP.
 AC V15732;
 DT 26-JUN-1998 (first entry)
 DE Primer P1W 316a for insulin analogue preparation.
 KW Insulin analogue; histidine-rich B-chain domain; treatment;
 KW diabetes; zinc-binding; delayed release; PCR primer;
 KW subcutaneous administration; ss.
 OS Synthetic.
 PN Homo sapiens.
 PN EP-821006-A2.
 PD 28-JAN-1998.
 PR 17-JUL-1997; 112197.
 PR 26-JUL-1996; DE-030242.
 PA (FARH) HOECHST AG.
 PI Ertl J, Geisen K, Habermann P, Seipke G;
 DR WPI; 98-102618/10.

PT Insulin analogues with histidine-rich B-chain domain - with high
 PT zinc-complexing capacity, useful for treatment of diabetes
 PS Example 3; Page 7; 22pp; German.
 CC The present sequence was used in the preparation of insulin
 CC analogues with a histidine-rich B-chain domain, which can be used in
 CC pharmaceutical formulations for treating diabetes. The analogues
 CC have a greater zinc-binding capacity than conventional forms of
 CC insulin, forming stable complexes having delayed release properties
 CC on subcutaneous administration. 4 A; 8 C; 16 G; 9 T;
 SQ Sequence 37 BP; 4 A; 8 C; 16 G; 9 T;
 Query Match 61.1%; Score 11; DB 41; Length 37;
 Best Local Similarity 92.3%; Pred. No. 8.84e+02;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Db 2 atcgagcatgat 14
 16 ATGCCTCATGAT 4
 Cp
 RESULT 22
 ID V51130 standard; DNA; 41 BP.
 AC V51130;
 DT 11-JAN-1999 (first entry)
 DE Maize polymorphic marker S26G5/G6-3 DNA.
 KW Polymorphic marker; allele-specific; primer; probe; amplification;
 KW hybridisation; plant; hybrid certification; genetic contribution;
 KW progeny; back cross; hybrid; ancestry; maize; ss.
 OS Zea mays.
 FH Key
 FT Location/Qualifiers
 FT variation
 FT /tag= "a"
 FT /replace= "a"
 FT /note= "polymorphism"
 PN WO9824796-A1.
 PD 11-JUN-1998.
 PR 01-DEC-1997; U21782.
 PR 07-MAR-1997; US-813507.
 PR 02-DEC-1996; US-032069.
 PA (AFPV-) AFFYMERIX INC.
 PI Landry BS, Lemieux B, Murgineux A, Sapolsky RJ;
 DR WPI; 98-33352/29.
 PT Brassica species allele-specific oligonucleotide probes and primers
 PT - useful for plant breeding
 PS Claim 1; Page 45; 65pp; English.
 CC This DNA sequence is a region of a Zea mays genome which contains a
 CC polymorphic marker. This sequence can be used in the construction of
 CC allele-specific primers and probes for amplification or hybridisation,
 CC e.g. to determine common or disparate ancestry between 2 or more plants,
 CC to monitor the genetic contribution of an ancestral plant, to trace the
 CC progeny of proprietary plants, in certification of a hybrid plant or to
 CC identify the progeny of a back-crossed plant with an ancestral plant.
 CC Sequence 41 BP; 11 A; 9 C; 12 T;
 SQ
 Query Match 61.1%; Score 11; DB 51; Length 41;
 Best Local Similarity 86.7%; Pred. No. 8.84e+02;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Db 15 tggccagatgattcc 29
 15 TGCCCTCATGATTC 1
 Cp
 RESULT 23
 ID V47878 standard; DNA; 41 BP.
 AC V47878;
 DT 14-OCT-1998 (first entry)
 DE Maize polymorphic site oligonucleotide marker UMC59-G5/G6-3.
 KW Maize; marker; probe; PCR primer; polymorphism; vegetal sequence;
 KW polymorphic site; corn; gramineae species; ss.
 OS Synthetic.
 PN Zea mays.
 PN WO9630717-A2.

PD 16-JUL-1998.
PF 02-DEC-1997; E07134.
PR 02-DEC-1996; US-032069.
PA (BIOC-) BIOCEM SA.
PI Murigneux A;
DR WPI: 98-399160/34.
PT Vegetal sequences including single nucleotide polymorphism - useful,
e.g. to determine polymorphisms in plants, determine strain in plant
breeding and to correlate polymorphisms with phenotypic traits
PS Claim 2; Page 14; 33pp; English.
CC The present invention describes a nucleic acid segment comprising at
least 10 contiguous nucleotides from a vegetal sequence including a
polymorphic site which is a single nucleotide polymorphism (SNP), or the
complement of the segment. Also described are: (1) an allele-specific
oligonucleotides hybridising to segment, or their complements, and (2) a
method of analysing nucleic acids from a subject, by determining if a
base is occupying any one (or a set) of polymorphic sites in 261.
CC sequences derived from six maize lines (see V47701 to V47961). The
CC segments are useful in fingerprint analysis in plants to determine which
CC polymorphisms are present, which strain a plant belongs to and to
CC distinguish between strains. The polymorphisms may correlate with
CC phenotypic traits (e.g. plant growth rate or crop yield), and the
CC segments are useful to determine the presence/absence of specific
CC polymorphisms correlating with the existence/absence of particular
CC traits. The segments are also useful in marker assisted back-cross
CC techniques to select plants with a higher percentage of recurrent parent
CC in a back-cross population. Segments incorporate SNPs which occur more
CC frequently than other polymorphism types and are therefore more likely to
CC be located close to genetic loci of interest; different forms of
CC polymorphism types. SNPs are also often easier to detect than other
SQ Sequence 41 BP; 11 A; 9 C; 8 G; 12 T;

Query Match 61.1%; Score 11; DB 46; Length 41;
Best Local Similarity 80.0%; Pred. No. 8.84e+02;
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 15 tgcacatgattcc 29
||| :|||
Cp 15 TGCCATGATGATCC 1

RESULT 24
ID V74222 standard; DNA; 19 BP.
AC V74222;
DT 15-MAR-1999 (first entry)
DE Cpg-N motif PCR primer Mu-15F.
KW Cpg-N motif; immunostimulation; antigen; Cpg-S motif; immunisation;
KW viral antigen; bacterial antigen; parasite; therapeutic; growth factor;
KW toxins; tumour suppressor; cytokine; apoptotic protein; interferon;
KW hormone; clotting factor; ligand; receptor; PCR primer; ss.
OS Synthetic.
PN WO9852581-A1.
PD 26-NOV-1998.
PF 20-MAY-1998; US-047233.
PR 20-MAY-1997; US-047209.
PA (OTTA-) OTTAMA CIVIC HOSPITAL LOEB RES INST.
PA (OIA-) OIAGEN GMBH.
PA (IOWA-) UNIV IOWA RES FOUND.
PI Davis Hl, Krieg AM, Schorr J, Wu T;
DR WPI: 99-059712/05.
PT Use of neutralising Cpg and stimulating Cpg motifs in DNA vectors -
PT enhancing the immunostimulatory effect of an antigen or
PT Example 1; Page 58; 109pp; English.
CC V74209-V74236 are PCR primers used to describe a method for enhancing the
CC immunostimulatory effect of an antigen encoded by nucleic acid contained
CC in a nucleic acid construct. The method involves determining the Cpg-N
CC and Cpg-S motifs present in the construct, removing neutralising Cpg-N
CC (Cpg-N) motifs and optionally inserting stimulatory Cpg (Cpg-S) motifs in
CC the construct, thereby producing a nucleic acid construct having enhanced
CC immunostimulatory efficacy. The method can be used for immunisation

CC against viral antigens, e.g. from hepatitis B virus (HBV), bacterial
CC antigens or an antigen derived from a parasite. They can also be used
CC for expression of a therapeutic polypeptide, e.g. growth factors, toxins,
CC tumour suppressors, cytokines, apoptotic proteins, interferons, hormones,
CC clotting factors, ligands and receptors.
SQ Sequence 19 BP; 1 A; 7 C; 5 G; 6 T;

Query Match 55.6%; Score 10; DB 59; Length 19;
Best Local Similarity 85.7%; Pred. No. 2.87e+03;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

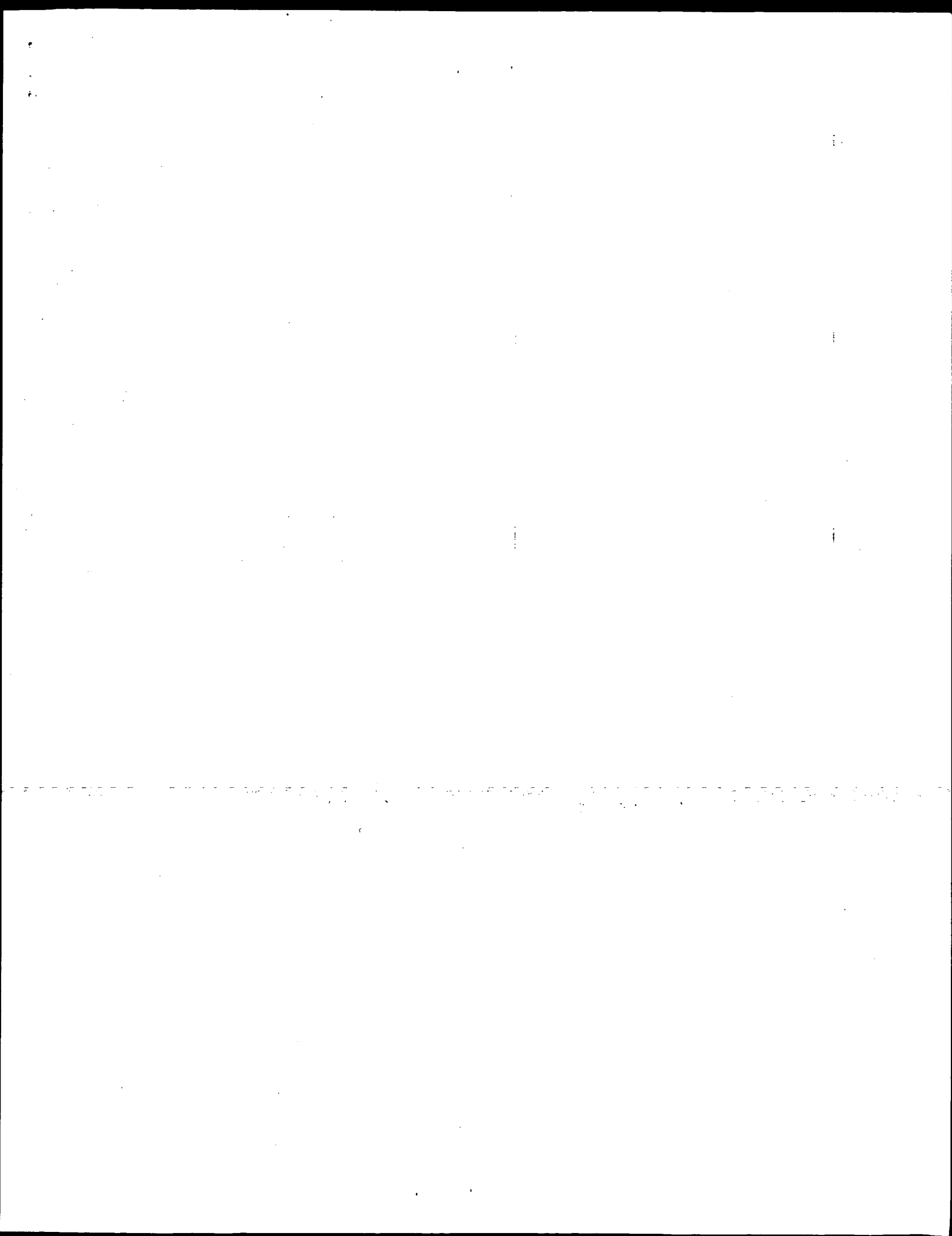
Db 3 gctcagcgttcc 16
||||| :|||
Cp 14 GCCTCATGATGATCC 1

RESULT 25
ID V99504 standard; DNA; 27 BP.
AC V99504;
DT 29-MAR-1999 (first entry)
DE T7 promoter/terminator PCR primer SM79.
KW Lysine; transgenic plant; seed storage protein; vector; psk5;
KW phage T7; promoter; terminator; PCR; primer; ss.
OS Synthetic.
PN WO9842831-A2.
PD 01-OCT-1998.
PF 27-MAR-1999; US-06051.
PR 27-MAR-1997; US-824627.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
PI Epebaum SU, Falco SC, McDevitt RE;
DR WPI: 99-045139/04.
PT Nucleic acids and chimeric genes for increasing seed lysine content
PT - comprise sequence encoding all or part of lysine ketoglutarate
PT reductase, useful to improve nutritional quality of seeds from
PT transformed plants
PS Example 21; Page 100; 231pp; English.
CC PCR primers SM79 and SM78 (see V99504) are designed to prime a
CC 300 base fragment from pMT430 spanning the T7 promoter and
CC terminator sequences. This fragment was used in the construction
CC of expression vector psk5. Chimeric genes for lysine-rich
CC synthetic seed storage proteins suitable for expression in the
CC seeds of plants have been constructed in psk5 (see V99513-18.
CC V99527-32, V99539-41). The invention also provides claimed
CC nucleic acids and chimeric genes useful for improving the
CC nutritional quality of seeds from transgenic plants. Methods
CC involve manipulation of lysine ketoglutarate reductase and
CC lysine-insensitive dihydrodipicolinic acid synthase activity (see
CC W87757-66).
SQ Sequence 27 BP; 6 A; 8 C; 8 G; 5 T;

Query Match 55.6%; Score 10; DB 60; Length 27;
Best Local Similarity 81.3%; Pred. No. 2.87e+03;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 8 atgcacatgattcc 23
||||| :|||
Cp 16 ATGCTCATGATGATCC 1

RESULT 26
ID Q36213 standard; DNA; 27 BP.
AC Q36213;
DT 25-MAY-1993 (first entry)
DE von Willebrand factor cDNA PCR primer.
KW von Willebrand factor; vascular disorders; prevention; treatment;
KW platelet aggregation; induction; inhibition; thrombosis;
KW polymerase chain reaction; ss.
OS Synthetic.
PN WO9300357-A.
PD 29-JAN-1993.
PF 29-JUN-1992; US-72.
PR 28-JUN-1991; US-20588.



CC TOPOLOGY: linear
SQ SEQUENCE 37 BP; 12 A; 8 C; 8 G; 9 T; 0 OTHER.

Query Match
Best Local Similarity 72.2%; Score 13; DB 2; Length 37;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 14 GGATCATCAGGATG 30
OY 1 GGATCATCAGGATG 17

RESULT 2
ID US-08-444-231-3 STANDARD; DNA; UNC; 37 BP.
AC xxxxxx

DE Sequence 3, Application US/08444231
CC Sequence 3, Application US/08444231
CC Patent No. 5652210
CC GENERAL INFORMATION:
CC APPLICANT: BARR, PHILIP J.
CC APPLICANT: SHAPIRO, JOHN P.
CC APPLICANT: KIEFER, MICHAEL C.
CC TITLE OF INVENTION: NOVEL FATE PROTEIN AND METHODS OF USE
CC TITLE OF INVENTION: THEREOF
CC NUMBER OF SEQUENCES: 22
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: MORRISON & FOERSTER
CC STREET: 755 Page Mill Road
CC City: Palo Alto
CC STATE: California
CC COUNTRY: USA
CC ZIP: 94304-1018
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.30
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/444,231
CC FILING DATE: 18-MAY-1995
CC CLASSIFICATION: 530
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/152,443
CC FILING DATE: 15-NOV-1993
CC ATTORNEY/AGENT INFORMATION:
CC NAME: LEHNHARDT, SUSAN K.
CC REGISTRATION NUMBER: 33,943
CC REFERENCE/DOCKET NUMBER: 23647-20006.00
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 813-5600
CC TELEFAX: (415) 494-0792
CC TELEX: 706141
CC INFORMATION FOR SEQ ID NO: 3:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 37 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
SQ SEQUENCE 37 BP; 12 A; 8 C; 8 G; 9 T; 0 OTHER.

Query Match
Best Local Similarity 72.2%; Score 13; DB 2; Length 37;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 14 GGATCATCAGGATG 30
OY 1 GGATCATCAGGATG 17

RESULT 3
ID PCT-US95-02521-1 STANDARD; DNA; UNC; 20 BP.
AC xxxxxx

DT Sequence 1, Application PC/TUS9502521
DE Sequence 1, Application PC/TUS9502521
CC GENERAL INFORMATION:
CC APPLICANT:
CC TITLE OF INVENTION: Methods for Identifying Genetic
CC TITLE OF INVENTION: Suppressor Elements and Genes Associated with Malignant
CC NUMBER OF SEQUENCES: 13
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US95/02521
CC FILING DATE:
CC INFORMATION FOR SEQ ID NO: 1:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 20 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: cDNA
SQ SEQUENCE 20 BP; 6 A; 2 C; 7 G; 5 T; 0 OTHER.

Query Match
Best Local Similarity 66.7%; Score 12; DB 4; Length 20;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 1 AATCATCGATGATG 16
OY 3 AATCATCGATGATG 18

RESULT 4
ID US-08-204-740-1 STANDARD; DNA; UNC; 20 BP.
AC xxxxxx

DE Sequence 1, Application US/08204740
CC Sequence 1, Application US/08204740
CC Patent No. 5753432
CC GENERAL INFORMATION:
CC APPLICANT: Gudkov, Andrei
CC APPLICANT: Kazarov, Alexander
CC APPLICANT: Mazo, Ilya
CC APPLICANT: Roninson, Igor B.
CC TITLE OF INVENTION: Methods for Identifying Genetic
CC TITLE OF INVENTION: Suppressor Elements and Genes Associated with Malignant
CC NUMBER OF SEQUENCES: 13
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Allgretti & Wilcoff, Ltd.
CC STREET: 10 S. Wacker Drive, Suite 3000
CC City: Chicago
CC STATE: Illinois
CC COUNTRY: USA
CC ZIP: 60606
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/204,740
CC FILING DATE: 04-MAR-1994
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: No. 5753432man, Kevin E
CC REGISTRATION NUMBER: 35,303
CC REFERENCE/DOCKET NUMBER: 93,354-C
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 312-715-1000

Mon Aug 2 13:58:59 1999

US-09-121-239-26.rn1

Page 3

CC TELEFAX: 312-715-1234
CC TELERX: 910-221-5317
CC INFORMATION FOR SEQ ID NO: 1:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 20 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: CDNA
SQ SEQUENCE 20 BP; 6 A; 2 C; 7 G; 5 T; 0 OTHER.

Query Match 66.7%; Score 12; DB 3; Length 20;
Best Local Similarity 87.5%; Pred. No. 4.58e+01;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 1 AATCATCGATGATCG 16
11111111111111111111
3 AATCATCGAGGCATCG 18

QY 3 AATCATCGAGGCATCG 18

RESULT 5
ID US-08-480-552-13 STANDARD; DNA; UNC; 20 BP.
AC xxxxxx
DE Sequence 13, Application US/08480552
CC Sequence 13, Application US/08480552
CC Patent No. 5665550
CC GENERAL INFORMATION:
CC APPLICANT: Gudkov, Andrei
CC TITLE OF INVENTION: Genes And Genetic Elements Associated
CC NUMBER OF SEQUENCES: 22
CC CORRESPONDENCE ADDRESS: 22
CC ADDRESSEE: Allegretti & Wilcoff, Ltd.
CC STREET: 75 State Street
CC CITY: Boston
CC STATE: Massachusetts
CC COUNTRY: U.S.A.
CC ZIP: 02109
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC OPERATING SYSTEM: IBM PC compatible
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/480,552
CC FILING DATE: 07-JUN-1995
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/033,086
CC FILING DATE: 09 MAR 1993
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Keown, Wayne A. 33, 923
CC REGISTRATION NUMBER: 93,354
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 617/345-9100
CC TELEFAX: 617/345-9111
CC INFORMATION FOR SEQ ID NO: 13:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 20 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: CDNA
CC HYPOTHETICAL: NO
CC ANTI-SENSE: NO
SQ SEQUENCE 20 BP; 6 A; 2 C; 7 G; 5 T; 0 OTHER.

Query Match 66.7%; Score 12; DB 2; Length 20;
Best Local Similarity 87.5%; Pred. No. 4.58e+01;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 1 AATCATCGATGATCG 16
11111111111111111111
3 AATCATCGAGGCATCG 18

QY 3 AATCATCGAGGCATCG 18

RESULT 6
ID PCT-US95-02303-1 STANDARD; DNA; UNC; 20 BP.
AC xxxxxx
DE Sequence 1, Application PC/TUS9502303
CC Sequence 1, Application PC/TUS9502303
CC GENERAL INFORMATION:
CC APPLICANT:
CC TITLE OF INVENTION: Genes and Genetic Elements Associated
CC NUMBER OF SEQUENCES: 25
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC OPERATING SYSTEM: IBM PC compatible
CC SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US95/02303
CC INFORMATION FOR SEQ ID NO: 1:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 20 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: CDNA
SQ SEQUENCE 20 BP; 6 A; 2 C; 7 G; 5 T; 0 OTHER.

Query Match 66.7%; Score 12; DB 4; Length 20;
Best Local Similarity 87.5%; Pred. No. 4.58e+01;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 1 AATCATCGATGATCG 16
11111111111111111111
3 AATCATCGAGGCATCG 18

QY 3 AATCATCGAGGCATCG 18

RESULT 7
ID US-08-480-552-14 STANDARD; DNA; UNC; 23 BP.
AC xxxxxx
DE Sequence 14, Application US/08480552
CC Sequence 14, Application US/08480552
CC Patent No. 5665550
CC GENERAL INFORMATION:
CC APPLICANT: Gudkov, Andrei
CC TITLE OF INVENTION: Genes And Genetic Elements Associated
CC NUMBER OF SEQUENCES: 22
CC CORRESPONDENCE ADDRESS: 22
CC ADDRESSEE: Allegretti & Wilcoff, Ltd.
CC STREET: 75 State Street
CC CITY: Boston
CC STATE: Massachusetts
CC COUNTRY: U.S.A.
CC ZIP: 02109
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC OPERATING SYSTEM: IBM PC compatible
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/480,552
CC FILING DATE: 07-JUN-1995
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/033,086

CC FILING DATE: 09 MAR 1993
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Keown, Wayne A.
CC REGISTRATION NUMBER: 33,923
CC REFERENCE/DOCKET NUMBER: 93,354
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 617/345-9100
CC TELEFAX: 617/345-9111
CC INFORMATION FOR SEQ ID NO: 14:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 23 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: cDNA
CC HYPOTHEICAL: NO
CC ANTI-SENSE: YES
CC SEQUENCE 23 BP; 8 A; 7 C; 2 G; 6 T; 0 OTHER.
SQ
Db Query Match 66.7%; Score 12; DB 2; Length 23;
Best Local Similarity 87.5%; Pred. No. 4.58e+01;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Cc 5 CCATCCATCGATGATT 20
18 CCATGCCCTCGATGATT 3
CP
DE RESULT 8
ID US-08-204-740-2 STANDARD; DNA; UNC; 23 BP.
AC xxxxxx
DT
CC Sequence 2, Application US/08204740
CC Patent No. 5753432
CC GENERAL INFORMATION:
CC APPLICANT: Gudkov, Andrei
CC APPLICANT: Kazarov, Alexander
CC APPLICANT: Mazo, Ilya
CC APPLICANT: Roninson, Igor B
CC TITLE OF INVENTION: Methods for Identifying Genetic
CC TITLE OF INVENTION: Suppressor Elements and Genes Associated with Malignant
CC NUMBER OF SEQUENCES: 13
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Allgretti & Wilcoff, Ltd.
CC STREET: 10 S. Wacker Drive, Suite 3000
CC CITY: Chicago
CC STATE: Illinois
CC COUNTRY: USA
CC ZIP: 60606
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/204,740
CC FILING DATE: 04-MAR-1994
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: NO. 5753432nan, Kevin E
CC REGISTRATION NUMBER: 35,303
CC REFERENCE/DOCKET NUMBER: 93,354-C
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 312-715-1234
CC TELEFAX: 312-715-1234
CC TELEFAX: 910-221-5317
CC INFORMATION FOR SEQ ID NO: 2:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 23 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single

CC TOPOLOGY: linear
CC MOLECULE TYPE: cDNA
CC SEQUENCE 23 BP; 8 A; 7 C; 2 G; 6 T; 0 OTHER.
SQ
Db Query Match 66.7%; Score 12; DB 3; Length 23;
Best Local Similarity 87.5%; Pred. No. 4.58e+01;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Cc 5 CCATCCATCGATGATT 20
18 CCATGCCCTCGATGATT 3
CP
DE RESULT 9
ID PCT-US95-02521-2 STANDARD; DNA; UNC; 23 BP.
AC xxxxxx
DT
CC Sequence 2, Application PC/TUS9502521
CC GENERAL INFORMATION:
CC APPLICANT:
CC TITLE OF INVENTION: Methods for Identifying Genetic
CC TITLE OF INVENTION: Suppressor Elements and Genes Associated with Malignant
CC NUMBER OF SEQUENCES: 13
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US95/02521
CC FILING DATE:
CC INFORMATION FOR SEQ ID NO: 2:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 23 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: cDNA
CC SEQUENCE 23 BP; 8 A; 7 C; 2 G; 6 T; 0 OTHER.
SQ
Db Query Match 66.7%; Score 12; DB 4; Length 23;
Best Local Similarity 87.5%; Pred. No. 4.58e+01;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Cc 5 CCATCCATCGATGATT 20
18 CCATGCCCTCGATGATT 3
CP
DE RESULT 10
ID PCT-US95-02303-2 STANDARD; DNA; UNC; 23 BP.
AC xxxxxx
DT
CC Sequence 2, Application PC/TUS9502303
CC GENERAL INFORMATION:
CC APPLICANT:
CC TITLE OF INVENTION: Genes and Genetic Elements Associated
CC TITLE OF INVENTION: with Sensitivity to Cisplatin
CC NUMBER OF SEQUENCES: 25
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US95/02303
CC INFORMATION FOR SEQ ID NO: 2:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 23 base pairs
CC TYPE: nucleic acid

CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: CDNA
SQ SEQUENCE 23 BP; 8 A; 7 C; 2 G; 6 T; 0 OTHER.

Query Match 66.7%; Score 12; DB 4; Length 23;
Best Local Similarity 87.5%; Pred. No. 4.58e+01;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 5 CCATCATGATGAT 20
||||| |||||||
CP 18 CCATCCTCATGAT 3

RESULT 11
ID PCT-US94-03437-87 STANDARD; DNA; UNC; 26 BP.
AC xxxxxx

DE Sequence 87, Application PC/TUS9403437.
CC Sequence 87, Application PC/TUS9403437.
CC GENERAL INFORMATION:
CC APPLICANT:
CC APPLICANT:
CC TITLE OF INVENTION: HOMOGENEOUS IMMUNOASSAYS USING MUTANT
CC TITLE OF INVENTION: GLUCOSE-6-PHOSPHATE DEHYDROGENASES
CC NUMBER OF SEQUENCES: 124
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US94/03437
CC FILING DATE:
CC INFORMATION FOR SEQ ID NO: 87:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 26 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: DNA (genomic)
CC HYPOTHETICAL: NO
CC ANTI-SENSE: NO
CC ORIGINAL SOURCE:
CC ORGANISM: Leuconostoc mesenteroides
CC STRAIN: ATCC 12291
SQ SEQUENCE 26 BP; 4 A; 8 C; 8 G; 6 T; 0 OTHER.

Query Match 61.1%; Score 11; DB 4; Length 26;
Best Local Similarity 92.3%; Pred. No. 1.83e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 TCATTGAGGATG 13
||||| |||||||
QY 5 TCATCGAGGATG 17

RESULT 12
ID US-08-463-953-37 STANDARD; DNA; UNC; 27 BP.
AC xxxxxx

DE Sequence 37, Application US/08463953
CC Sequence 37, Application US/08463953
CC Patent No. 5502034
CC GENERAL INFORMATION:
CC APPLICANT: Holly, Richard D.
CC APPLICANT: Foster, Donald C.
CC TITLE OF INVENTION: METHODS FOR PRODUCING THROMBIN
CC NUMBER OF SEQUENCES: 48
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Townsend and Townsend
CC STREET: One Market Plaza, Stewart Street Tower,
CC STREET: Twentieth floor

CC CITY: San Francisco
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 94105

CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/463,953
CC FILING DATE:
CC CLASSIFICATION: 514
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/860,701
CC FILING DATE: 31-MAR-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/816,281
CC FILING DATE: 31-DEC-1991
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Patmelee, Steven W.
CC REGISTRATION NUMBER: 31,990
CC REFERENCE/DOCKET NUMBER: 13952-12-2
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 206-467-9600
CC TELEFAX: 415-543-5043
CC INFORMATION FOR SEQ ID NO: 37:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 27 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC IMMEDIATE SOURCE:
CC CLONE: ZC1551
SQ SEQUENCE 27 BP; 4 A; 9 C; 10 G; 4 T; 0 OTHER.

Query Match 61.1%; Score 11; DB 1; Length 27;
Best Local Similarity 92.3%; Pred. No. 1.83e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 15 TCCTCGAGGATG 27
||||| |||||||
QY 5 TCATCGAGGATG 17

RESULT 13
ID PCT-US93-12687-7 STANDARD; DNA; UNC; 27 BP.
AC xxxxxx

DE Sequence 7, Application PC/TUS9312687
CC Sequence 7, Application PC/TUS9312687
CC GENERAL INFORMATION:
CC APPLICANT: Iranli, Meher H.
CC TITLE OF INVENTION: HYBRID CROSS-LINKING PROTEINS
CC NUMBER OF SEQUENCES: 14
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Zymogenetics, Inc.
CC STREET: 4225 Roosevelt Way, N.E.
CC CITY: Seattle
CC STATE: WA
CC COUNTRY: USA
CC ZIP: 98105

CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US93/12687
CC FILING DATE:
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/998,271

CC FILING DATE: 31-DEC-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Parker, Gary E
CC REGISTRATION NUMBER: 31-648
CC REFERENCE/DOCKET NUMBER: 92-26PC
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 206-547-8080 ext 322
CC TELEFAX: 206-548-2329
CC INFORMATION FOR SEQ ID NO: 7:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 27 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC IMMEDIATE SOURCE:
CC CLONE: ZC1551
CC
SQ SEQUENCE 27 BP; 4 A; 9 C; 10 G; 4 T; 0 OTHER.

Query Match 61.1%; Score 11; DB 4; Length 27;
Best Local Similarity 92.3%; Pred. No. 1.83e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 15 TCCTCGAGGCAATG 27
|||
OY 5 TCATCGAGGCAATG 17

RESULT 14
ID US-07-998-972A-37 STANDARD; DNA; UNC; 27 BP.
AC xxxxxx

Sequence 37, Application US/07998972A
Sequence 37, Application US/07998972A
Patent No. 5476777
GENERAL INFORMATION:
APPLICANT: Holly, Richard D.
APPLICANT: Foster, Donald C.
TITLE OF INVENTION: METHODS FOR PRODUCING THROMBIN
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend
STREET: One Market Plaza, Stewart Street Tower,
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/998,972A
FILING DATE: 19921230
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/860,701
FILING DATE: 31-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/816,281
FILING DATE: 31-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 13952-12-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-5043
TELEFAX: 206-467-9600
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
TYPE: nucleic acid

CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC IMMEDIATE SOURCE:
CC CLONE: ZC1551
SQ SEQUENCE 27 BP; 4 A; 9 C; 10 G; 4 T; 0 OTHER.

Query Match 61.1%; Score 11; DB 1; Length 27;
Best Local Similarity 92.3%; Pred. No. 1.83e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 15 TCCTCGAGGCAATG 27
|||
OY 5 TCATCGAGGCAATG 17

RESULT 15
ID US-08-462-261-37 STANDARD; DNA; UNC; 27 BP.
AC xxxxxx

Sequence 37, Application US/08462261
Sequence 37, Application US/08462261
Patent No. 5527692
GENERAL INFORMATION:
APPLICANT: Holly, Richard D.
APPLICANT: Foster, Donald C.
TITLE OF INVENTION: METHODS FOR PRODUCING THROMBIN
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend
STREET: One Market Plaza, Stewart Street Tower,
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,261
FILING DATE: 05-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/998,972
FILING DATE: 30-DEC-1992
APPLICATION NUMBER: US 07/860,701
FILING DATE: 31-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/816,281
FILING DATE: 31-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 13952-12-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-5043
TELEFAX: 206-467-9600
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: ZC1551
SQ SEQUENCE 27 BP; 4 A; 9 C; 10 G; 4 T; 0 OTHER.

Query Match 61.1%; Score 11; DB 1; Length 27;
Best Local Similarity 92.3%; Pred. No. 1.83e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
CC TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-6
CC NUMBER OF SEQUENCES: 21
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Spensley Horn Jubas & Lubitz
CC STREET: 1880 Century Park East, Suite 500
CC CITY: Los Angeles
CC STATE: California
CC COUNTRY: USA
CC ZIP: 90067
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US94/07762
CC FILING DATE: 08-JUL-1994
CC CLASSIFICATION:
CC ATTORNEY/AGENT INFORMATION:
CC NAME: TOMARIN, LISA A., PH.D.
CC REGISTRATION NUMBER: P-38,347
CC REFERENCE/DOCKET NUMBER: FD2349
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (619) 455-5110
CC TELEFAX: (619) 455-5110
CC INFORMATION FOR SEQ ID NO: 2:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 33 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: DNA (genomic)
CC IMMEDIATE SOURCE:
CC CLONE: SJL145
CC FEATURE:
CC
CC NAME/KEY: CDS
CC LOCATION: 1..29
CC OTHER INFORMATION: S/note= "R-adenine or guanine;
CC OTHER INFORMATION: N-cytosine or guanine; M-adenine or cytosine;
CC OTHER INFORMATION: N-adenine cytosine, guanine or thymine;
CC OTHER INFORMATION: Y-cytosine or thymine; B-Inosine"
CC
CC SEQUENCE 33 BP: 6 A; 9 C; 3 G; 4 T; 11 OTHER.
CC
Db Query Match 61.1%; Score 11; DB 4; Length 33;
Best Local Similarity 42.9%; Pred. NO. 1.35e+02;
Matches 6; Conservative 6; Mismatches 2; Indels 0; Gaps 0.
Cc 17 CABGMNTCBAJRY 30
|||: |||:::
17 CATGCCCTCATGAT 4
RESULT 18
US-08-455-559-6 STANDARD; DNA; UNC; 33 BP.
AC xxxxxx
DT Sequence 6, Application US/08455559
DE Sequence 6, Application US/08455559
Cc Patent No. 5801014
CC GENERAL INFORMATION:
CC APPLICANT: LEE, SE-JIN
CC APPLICANT: HUYNH, THANH
CC TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-5
CC NUMBER OF SEQUENCES: 27
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: SPENSLEY HORN JUBAS & LUBITZ
CC STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
CC CITY: LOS ANGELES
CC STATE: CALIFORNIA
CC COUNTRY: US
CC ZIP: 90067
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
```


Mon Aug 2 13:58:59 1999

US-09-121-239-26.rni

Page 9

CC TITLE OF INVENTION: INHIBITING APOLIPOPROTEIN
CC... TITLE OF INVENTION:
CC NUMBER OF SEQUENCES: 392
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Lyon & Lyon
CC STREET: 633 West Fifth Street
CC CITY: Suite 4700
CC City: Los Angeles
CC STATE: California
CC COUNTRY: U.S.A.
CC ZIP: 90071
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
CC MEDIUM TYPE: Storage
CC COMPUTER: IBM Compatible
CC OPERATING SYSTEM: IBM P.C. DOS 5.0
CC SOFTWARE: FASTSEQ Version 1.5
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/311,760A
CC FILING DATE: September 23, 1994
CC Prior Application Data:
CC APPLICATION NUMBER:
CC FILING DATE:
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Warburg, Richard
CC REGISTRATION NUMBER: 32,327
CC REFERENCE/DOCKET NUMBER: 208/155
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (213) 489-1600
CC TELEFAX: (213) 955-0440
CC TELEX: 67-3510
CC INFORMATION FOR SEQ. ID NO.: 176:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 15 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC SEQUENCE 15 BP; 4 A; 3 C; 5 G; 0 T; 3 OTHER.

Dt Query Match 55.6%; Score 10; DB 1; Length 15;
Best Local Similarity 71.4%; Pred.No. 6.87e+02;
Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0.

Oy 1 GAGUUAUCGAGCA 14
|| : |||||||
2 GAATCATCGAGCA 15

RESULT 22
ID US-08-311-760A-9 STANDARD; DNA; UNC; 15 BP.
AC xxxxxx
DT Sequence 9, Application US/08311760A
DE Sequence 9, Application US/08311760A
CC Patent No. 5599706
CC GENERAL INFORMATION:
CC APPLICANT: Stinchcomb, Jan T.
CC APPLICANT: McSwigen, James
CC APPLICANT: Newton, Roger S.
CC APPLICANT: Rambarack, Randy
CC TITLE OF INVENTION: RIBOZYME TREATMENT OF DISEASES
CC TITLE OF INVENTION: OR CONDITIONS RELATED TO LEVELS OF
CC TITLE OF INVENTION: PLASMA LIPOPROTEIN (a) [LP(a)] BY
CC TITLE OF INVENTION: INHIBITING APOLIPOPROTEIN
CC NUMBER OF SEQUENCES: 392
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Lyon & Lyon
CC STREET: 633 West Fifth Street
CC CITY: Suite 4700
CC City: Los Angeles
CC STATE: California
CC COUNTRY: U.S.A.

```
CC      ZIP: 90071
CC      COMPUTER READABLE FORM:
CC      MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
CC      MEDIUM TYPE: storage
CC      COMPUTER: IBM Compatible
CC      OPERATING SYSTEM: IBM P.C. DOS 5.0
CC      SOFTWARE: FastSeq Version 1.5
CC      CURRENT APPLICATION DATA:
CC      APPLICATION NUMBER: US/08/311,760A
CC      FILING DATE: September 23, 1994
CC      PRIOR APPLICATION DATA:
CC      APPLICATION NUMBER:
CC      FILING DATE:
CC      ATTORNEY/AGENT INFORMATION:
CC      NAME: Waiburg, Richard
CC      REGISTRATION NUMBER: 32,327
CC      REFERENCE/DOCKET NUMBER: 208/155
CC      TELECOMMUNICATION INFORMATION:
CC      TELEPHONE: (213) 489-1600
CC      TELEFAX: (213) 955-0440
CC      TELEX: 67-3510
CC      INFORMATION FOR SEQ ID NO: 9:
CC      SEQUENCE CHARACTERISTICS:
CC      LENGTH: 15 base pairs
CC      type: nucleic acid
CC      STRANDEDNESS: single
CC      TOPOLOGY: linear
CC      SEQUENCE 15 BP; 4 A; 3 C; 5 G; 0 T; 3 OTHER.
SQ
Query Match          55.6%; Score 10; DB 1; Length 15;
Best Local Similarity 71.4%; Pred.No. 6.87e+02;
Matches    10; Conservative    2; Mismatches    2; Indels    0; Gaps    0;

Db      1 GAGUUAUCGAGCA 14
        || : | : |||||
Oy      2 GAATCATCGAGCA 15

RESULT   23
ID       US-07-855-417A-12 STANDARD; DNA; UNC; 20 BP.
AC       xxxxxx
DE       Sequence 12, Application US/07855417A
CC       Sequence 12, Application US/07855417A
CC       Patent No. 5484885
CC       GENERAL INFORMATION:
CC       APPLICANT: Perella, Heloise Anne
CC       TITLE OF INVENTION: Chemotactic, Antibiotic and
CC       TITLE OF INVENTION: Lipopolysaccharide-Binding Peptide Fragments of CAP37
CC       NUMBER OF SEQUENCES: 29
CC       CORRESPONDENCE ADDRESS:
CC       ADDRESSEE: Needle & Rosenberg, P.C.
CC       STREET: 133 Carnegie Way N.W., Suite 400
CC       CITY: Atlanta
CC       STATE: Georgia
CC       COUNTRY: USA
CC       ZIP: 30303
CC       COMPUTER READABLE FORM:
CC       MEDIUM TYPE: Floppy disk
CC       COMPUTER: IBM PC compatible
CC       OPERATING SYSTEM: PC-DOS/MS-DOS
CC       SOFTWARE: Patentin Release #1.0, Version #1.25
CC       CURRENT APPLICATION DATA:
CC       APPLICATION NUMBER: US/07/855,417A
CC       FILING DATE: 18-MAR-1992
CC       CLASSIFICATION: 435
CC       PRIOR APPLICATION DATA:
CC       APPLICATION NUMBER: US 07/543,151
CC       FILING DATE: 25-JUN-1990
CC       PRIOR APPLICATION DATA:
CC       APPLICATION NUMBER: US 07/375,739
CC       FILING DATE: 05-JUL-1989
```

CC ATTORNEY/AGENT INFORMATION:
CC NAME: Severson, Mary L.
CC REGISTRATION NUMBER: 34,927
CC REFERENCE/DOCKET NUMBER: 0510.024
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (404) 688-0770
CC TELEFAX: (404) 688-9880
CC INFORMATION FOR SEQ ID NO: 12:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 20 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: DNA (genomic)
CC SEQUENCE 20 BP; 1 A; 5 C; 3 G; 6 T; 5 OTHER.
SQ
Db 2 UGCCTCCYGRTTY 15
:||||| 11:11:
Cp 15 TGCCTCGATGATTC 2
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
Db 2 UGCCTCCYGRTTY 15
:||||| 11:11:
Cp 15 TGCCTCGATGATTC 2
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
RESULT 24
ID US-07-969-931-12 STANDARD; DNA; UNC; 20 BP.
AC xxxxxx
DE Sequence 12, Application US/07969931
CC Sequence 12, Application US/07969931
CC Patent No. 5458874
CC GENERAL INFORMATION:
CC APPLICANT: Pereira, Heloise Anne
CC APPLICANT: Spitznagel, John K.
CC TITLE OF INVENTION: Chemotactic, Antibiotic and
CC TITLE OF INVENTION: Lipopolysaccharide-Binding Peptide Fragments of CAP37
CC NUMBER OF SEQUENCES: 29
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Needle & Rosenberg, P.C.
CC STREET: 133 Carnegie Way N.W., Suite 400
CC CITY: Atlanta
CC STATE: Georgia
CC COUNTRY: USA
CC ZIP: 30303
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/07/969,931
CC FILING DATE: 19921030
CC CLASSIFICATION: 514
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/543,151
CC FILING DATE: 25-JUN-1990
CC APPLICATION NUMBER: US 07/543,151
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/375,739
CC FILING DATE: 05-JUL-1989
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Severson, Mary L.
CC REGISTRATION NUMBER: 34,927
CC REFERENCE/DOCKET NUMBER: 0510.024
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (404) 688-0770
CC TELEFAX: (404) 688-9880
CC INFORMATION FOR SEQ ID NO: 12:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 20 base pairs
CC TYPE: NUCLEIC ACID
CC STRANDEDNESS: single
CC TOPOLOGY: linear

CC MOLECULE TYPE: DNA (genomic)
SQ SEQUENCE 20 BP; 1 A; 5 C; 3 G; 6 T; 5 OTHER.
Query Match 55.6%; Score 10; DB 1; Length 20;
Best Local Similarity 64.3%; Pred. No. 6.87e+02;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
Db 2 UGCCTCCYGRTTY 15
:||||| 11:11:
Cp 15 TGCCTCGATGATTC 2
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
RESULT 25
ID PCT-US96-09455A-61 STANDARD; DNA; UNC; 21 BP.
AC xxxxxx
DE Sequence 61, Application PC/TUS9609455A
CC Sequence 61, Application PC/TUS9609455A
CC GENERAL INFORMATION:
CC APPLICANT: PARMA, et al.
CC TITLE OF INVENTION: HIGH AFFINITY NUCLEIC ACID
CC TITLE OF INVENTION: LIGANDS TO LECTINS
CC NUMBER OF SEQUENCES: 390
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Swanson & Bratschun, L.L.C.
CC STREET: 18400 E. Prentice Avenue, Suite 200
CC CITY: Englewood
CC STATE: Colorado
CC COUNTRY: USA
CC ZIP: 80111
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MB
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: MS-DOS
CC SOFTWARE: Wordperfect 6.0
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US96/09455A
CC FILING DATE: 05 JUNE 1996
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 08/479,724
CC FILING DATE: 07-JUNE-1995
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 08/472,256
CC FILING DATE: 07-JUNE-1995
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 08/472,255
CC FILING DATE: 07-JUNE-1995
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 08/477,829
CC FILING DATE: 07-JUNE-1995
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Barry J. Swanson
CC REGISTRATION NUMBER: 33,215
CC REFERENCE/DOCKET NUMBER: NEX40C/PCT
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (303) 793-3333
CC TELEFAX: (303) 793-3433
CC INFORMATION FOR SEQ ID NO: 61:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 21 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: RNA
CC FEATURE:
CC OTHER INFORMATION: All C's are 2'-NH2 cytosine
CC FEATURE:
CC OTHER INFORMATION: All U's are 2'-NH2 uracil
SQ SEQUENCE 21 BP; 2 A; 3 C; 8 G; 0 T; 8 OTHER.
Query Match 55.6%; Score 10; DB 4; Length 21;
Best Local Similarity 50.0%; Pred. No. 6.87e+02;

Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Db 8 UGACYCGGAGAYUC 21
: | | | | | | | | | |
Cp 15 TGCCTCGATGATTC 2

RESULT 26
ID US-08-479-724A-61 STANDARD; DNA; UNC; 21 BP.
AC xxxxxx

DE Sequence 61, Application US/08479724A
CC Sequence 61, Application US/08479724A
CC Patent No. 5780228
CC GENERAL INFORMATION:
CC APPLICANT: PARMA, DAVID
CC TITLE OF INVENTION: HIGH AFFINITY NUCLEIC ACID LIGANDS
CC TITLE OF INVENTION: TO LECTINS
CC NUMBER OF SEQUENCES: 173
CC CORRESPONDENCE ADDRESSES:
CC ADDRESSEE: Swanson & Bratschun, L.L.C.
CC STREET: 8400 E. Prentice Avenue, Suite 200
CC City: Englewood
CC STATE: Colorado
CC COUNTRY: USA
CC ZIP: 80111

CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MB
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: MS-DOS
CC SOFTWARE: WordPerfect 6.0
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/479,724A
CC FILING DATE: 07-JUNE-1995
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 07/714,131
CC FILING DATE: 10-JUNE-1991
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 07/536,428
CC FILING DATE: 11-JUNE-1991
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 07/964,624
CC FILING DATE: 21-OCTOBER-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Barry J. Swanson
CC REGISTRATION NUMBER: 33,215
CC REFERENCE/DOCKET NUMBER: NEX40-1
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (303) 793-3333
CC TELEFAX: (303) 793-3433
CC INFORMATION FOR SEQ ID NO: 61:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 21 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: RNA
CC FEATURE:
CC OTHER INFORMATION: All C's are 2'-NH2 cytosine
CC FEATURE:
CC OTHER INFORMATION: All U's are 2'-NH2 uracil
CC SEQUENCE 21 BP; 2 A; 3 C; 8 G; 0 T; 8 OTHER.

Query Match 55.6%; Score 10; DB 3; Length 21;
Best Local Similarity 50.0%; Pred. No. 6.87e+02;
Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Db 8 UGACYCGGAGAYUC 21
: | | | | | | | | | |
Cp 15 TGCCTCGATGATTC 2

RESULT 27
ID US-08-181-556-11 STANDARD; DNA; UNC; 23 BP.
AC xxxxxx

DE Sequence 11, Application US/08181556
CC Sequence 11, Application US/08181556
CC Patent No. 5525486
CC GENERAL INFORMATION:
CC APPLICANT: HONJO, Tasuku
CC APPLICANT: TASHIRO, Kei
CC TITLE OF INVENTION: PROCESS FOR CONSTRUCTING CDNA LIBRARY,
CC TITLE OF INVENTION: AND NOVEL POLYPEPTIDE AND DNA CODING FOR THE SAME
CC NUMBER OF SEQUENCES: 11
CC CORRESPONDENCE ADDRESSES:
CC ADDRESSEE: STEVENS, DAVID, MILLER & MOSHER
CC STREET: 515 No. 5525486th Washington Street (P.O. Box 1427)
CC City: Alexandria
CC STATE: Virginia
CC COUNTRY: USA
CC ZIP: 22313

CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/181,556
CC FILING DATE: 14-JAN-1994
CC CLASSIFICATION: 424
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: JP 5-22098
CC FILING DATE: 14-JAN-1993
CC ATTORNEY/AGENT INFORMATION:
CC NAME: POTIOS III, James A.
CC REGISTRATION NUMBER: 31714
CC REFERENCE/DOCKET NUMBER: TTP/29088
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (703) 549-7200
CC TELEFAX: (703) 528-5313
CC TELEX: 89-2746

CC INFORMATION FOR SEQ ID NO: 11:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 23 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: cDNA to mRNA
CC FEATURE:
CC NAME/KEY: modified_base
CC LOCATION: 1..23
CC OTHER INFORMATION: /note="A 17 mer da ligated to a
CC OTHER INFORMATION: restriction enzyme site containing EcoRI (the 3'
CC OTHER INFORMATION: end)." end)
CC SEQUENCE 23 BP; 4 A; 8 C; 8 G; 3 T; 0 OTHER.

Query Match 55.6%; Score 10; DB 1; Length 23;
Best Local Similarity 85.7%; Pred. No. 6.87e+02;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 10 GCCTCGAGATTC 23
: | | | | | | | | | |
Cp 14 GCCTCGATGATTC 1

RESULT 28
ID US-08-474-633A-19 STANDARD; DNA; UNC; 27 BP.
AC xxxxxx

DE Sequence 19, Application US/08474633A
CC Sequence 19, Application US/08474633A
CC Patent No. 5773691

```
CC GENERAL INFORMATION:
CC APPLICANT: E. I. DU PONT DE NEMOURS AND
CC APPLICANT: COMPANY
CC TITLE OF INVENTION: CHIMERIC GENES AND
CC TITLE OF INVENTION: METHODS FOR INCREASING
CC TITLE OF INVENTION: INCREASING THE LYSINE
CC TITLE OF INVENTION: AND THREONINE CONTENT
CC TITLE OF INVENTION: OF THE SEEDS OF PLANTS
CC NUMBER OF SEQUENCES: 107
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: E. I. DU PONT DE NEMOURS
CC ADDRESSEE: AND COMPANY
CC STREET: 1007 MARKET STREET
CC CITY: WILMINGTON
CC STATE: DELAWARE
CC COUNTRY: U.S.A.
CC ZIP: 19898
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: FLOPPY DISK
CC COMPUTER: IBM PC COMPATIBLE
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: MICROSOFT WORD VERSION 2.0C
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/474,633A
CC FILING DATE:
CC CLASSIFICATION: 800
CC ATTORNEY/AGENT INFORMATION:
CC NAME: BARBARA C. STEGELL
CC REGISTRATION NUMBER: 30,684
CC REFERENCE/DOCKET NUMBER: BB-1037-C
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 302-992-4931
CC TELEFAX: 302-773-0164
CC TELEX: 835420
CC INFORMATION FOR SEQ ID NO: 19:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 27 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: DNA (genomic)
CC FEATURE:
CC NAME/KEY: misc_feature
CC LOCATION: 1..27
CC OTHER INFORMATION: /product= "synthetic
CC OTHER INFORMATION: oligonucleotide"
CC OTHER INFORMATION: /standard_name= "SM
CC OTHER INFORMATION: 79"
CC SEQUENCE 27 BP; 6 A; 8 C; 8 G; 5 T; 0 OTHER.
SQ
Query Match 55.6%; Score 10; DB 3; Length 27;
Best Local Similarity 81.3%; Pred. No. 6.87e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0;
Gb 0;
Db 8 ATGCCACGATCGCTCC 23
||||| ||||| |||
| | | | |
Cc 16 ATGCCTCATGATTTC 1
RESULT 29
ID US-08-182-175A-12 STANDARD: DNA; UNC: 27 BP.
AC xxxxxx
DT
DE Sequence 12, Application US/08182175A
CC Sequence 12, Application US/08182175A
CC Patent No. 5559223
CC GENERAL INFORMATION:
CC APPLICANT: Saverio Carl Falco
CC APPLICANT: Sharon J. Keeler
CC APPLICANT: Janet A. Rice
CC TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containing
CC NUMBER OF SEQUENCES: 113
CC CORRESPONDENCE ADDRESS:
```

```

CC ADDRESSÉE: E.I. du Pont de Nemours and Company
CC STREET: 1007 Market Street
CC CITY: Wilmington
CC STATE: Delaware
CC COUNTRY: USA
CC ZIP: 19898
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy Disk
CC COMPUTER: Macintosh
CC OPERATING SYSTEM: Macintosh System, 6.0
CC SOFTWARE: Microsoft Word, 4.0
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/182,175A
CC FILING DATE:
CC CLASSIFICATION: 800
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 07/743, 006
CC FILING DATE: 9 August 1991
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Linda Axamethy Floyd
CC REGISTRATION NUMBER: 33,692
CC REFERENCE/DOCKET NUMBER: BB-1031
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (302) 992-4929
CC TELEFAX: (302) 892-7949
CC INFORMATION FOR SEQ ID NO: 12:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 27 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: DNA (genomic)
CC FEATURE:
CC NAME/KEY: misc_feature
CC LOCATION: 1..27
CC OTHER INFORMATION: /product="synthetic oligonucleotide"
CC OTHER INFORMATION: /standard_name="SM 7g"
CC SEQ SEQUENCE 27 BP; 6 A; 8 C; 8 G; 5 T; 0 OTHER.

Query Match 55.6%; Score 10; DB 1; Length 27;
Best Local Similarity 81.3%; Pred. No. 6,87e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 8 ATGCCAGCATGCGTCC 23
16 ATGCTCGATGATGTC 1

RESULT 30
ID PCT-US92-06412-12 STANDARD; DNA; UNC; 27 BP.
AC xxxxxx
DE Sequence 12, Application PC/TUS9206412
CC Sequence 12, Application PC/TUS9206412
CC GENERAL INFORMATION:
CC APPLICANT: Saverio Carl Falco
CC APPLICANT: Sharon J. Keeler
CC APPLICANT: Janet A. Rice
CC TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Contain
CC NUMBER OF SEQUENCES: 113
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: E.I. du Pont de Nemours and Company
CC STREET: 1007 Market Street
CC CITY: Wilmington
CC STATE: Delaware
CC COUNTRY: USA
CC ZIP: 19898
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy Disk
CC COMPUTER: Macintosh
CC OPERATING SYSTEM: Macintosh System, 6.0
CC SOFTWARE: Microsoft Word, 4.0

```

```

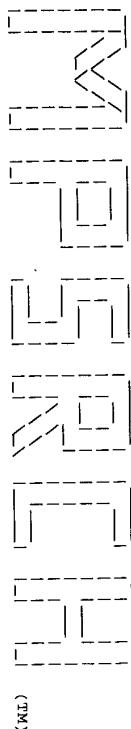
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US92/06412
CC FILING DATE: 19920807
CC CLASSIFICATION: 530
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 07/743,006
CC FILING DATE: 9 August 1991
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Linda Axamechy Floyd
CC REGISTRATION NUMBER: 33,692
CC REFERENCE/DOCKET NUMBER: BB-1031
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (302) 992-4929
CC TELEFAX: (302) 892-7949
CC TELEX: 835420
CC INFORMATION FOR SEQ. ID NO: 12:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 27 base pairs
CC TYPE: NUCLEIC ACID
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: DNA (genomic)
CC FEATURE:
CC NAME/KEY: misc_feature
CC LOCATION: 1..27
CC OTHER INFORMATION: /product= "synthetic oligonucleotide"
CC OTHER INFORMATION: /standard_name= "SM 79"
SQ SEQUENCE 27 BP; 6 A; 8 C; 8 G; 5 T; 0 OTHER.

Query Match 55.6%; Score 10; DB 4; Length 27;
Best Local Similarity 81.3%; Pred. No. 6.87e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 8 ATGCCAGATCGCTCC 23
CP 16 ATGCTCGATGATTC 1

Search completed: Mon Aug 2 12:14:52 1999
Job time : 82 secs.

```

Release 3.1A John F. Collins, Biocomputing Research Unit.
Copyright (c) 1993-1998 University of Edinburgh, U.K.
Distribution rights by Oxford Molecular Ltd

Mpsrch_un n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Mon Aug 2 12:09:45 1999; Maspar time 135.39 Seconds
311.525 Million cell updates/sec

Tabular output not generated.

Title: >US-09-121-239-26
Description: (1-18) from US09121239.seq
Percent Score: 18
N.A. Sequence: 1 GGATCATCGAGGATG 18
Comp: CCTACTAGCTCCCTACC

Scoring table: TABLE default
Gap 10

Nmatch STD: Dbase 0; Query 0

Searched: 2883791 seqs, 1171580779 bases x 2

Post-processing: Minimum Match 0%
Listing first 1000 summaries
Maximum DB seq length 50

Database: emb1-est58
1:em_est10 2:em_est11 3:em_est17 4:em_est18 5:em_est12
6:em_est19 7:em_gss1
genbank-est111
8:gb_est1 9:gb_est10 10:gb_est11 11:gb_est12 12:gb_est13
13:gb_est14 14:gb_est15 15:gb_est16 16:gb_est17
17:gb_est18 18:gb_est19 19:gb_est20 20:gb_est21
21:gb_est22 22:gb_est23 23:gb_est24 24:gb_est25
25:gb_est26 26:gb_est27 27:gb_est28 28:gb_est29
29:gb_est30 30:gb_est31 31:gb_est32 32:gb_est33 33:gb_est34
34:gb_est35 35:gb_est36 36:gb_est37 37:gb_gss1 38:gb_gss2
39:gb_gss3 40:gb_gss4 41:gb_gss5 42:gb_gss6

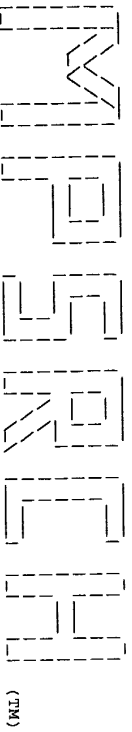
Statistics: Mean 6.252; Variance 1.127; scale 5.546

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
No matches found.						

Search completed: Mon Aug 2 12:14:48 1999
Job time : 303 secs.



Release 3.1A John F. Collins, Biocomputing Research Unit.
Copyright (c) 1993-1998 University of Edinburgh, U.K.
Distribution rights by Oxford Molecular Ltd

Msrch_mn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Mon Aug 2 12:19:42 1999; Maspar time 133.50 Seconds
539,865 Million cell updates/sec

Tabular output not generated.

Title: >US-09-121-239-27
Description: (1-26) from US09121239.seq
Perfect Score: 26
N.A. Sequence: 1 CACTCAGCCACCTGCGATTACAGAG 26
Comp: GTGAGTGGGTGACCTAAATGCTCTC

Scoring table: TABLE default
Gap 10

Nmatch STD : Dbase 0; Query 0

Searched: 646147 segs, 1385953633 bases x 2

Post-processing: Minimum Match 0%
Listing first 1000 summaries
Maximum DB seq length 50

Database: emb158
1:em_ba1 2:em_ba2 3:em_fun 4:em_htg 5:em_hum1 6:em_hum2
7:em_in 8:em_cm 9:em_ov 10:em_pat 11:em_ph
13:em_pl 14:em_ro 15:em_sts 16:em_vl
genbank11
17:gb_ba1 18:gb_ba2 19:gb_htg1 20:gb_htg2 21:gb_in1
22:gb_in2 23:gb_cm 24:gb_ov 25:gb_pat 26:gb_ph 27:gb_pl1
28:gb_pl2 29:gb_pl3 30:gb_pr2 31:gb_pr3 32:gb_ro
33:gb_st 34:gb_sts 35:gb_sy 36:gb_un 37:gb_vl

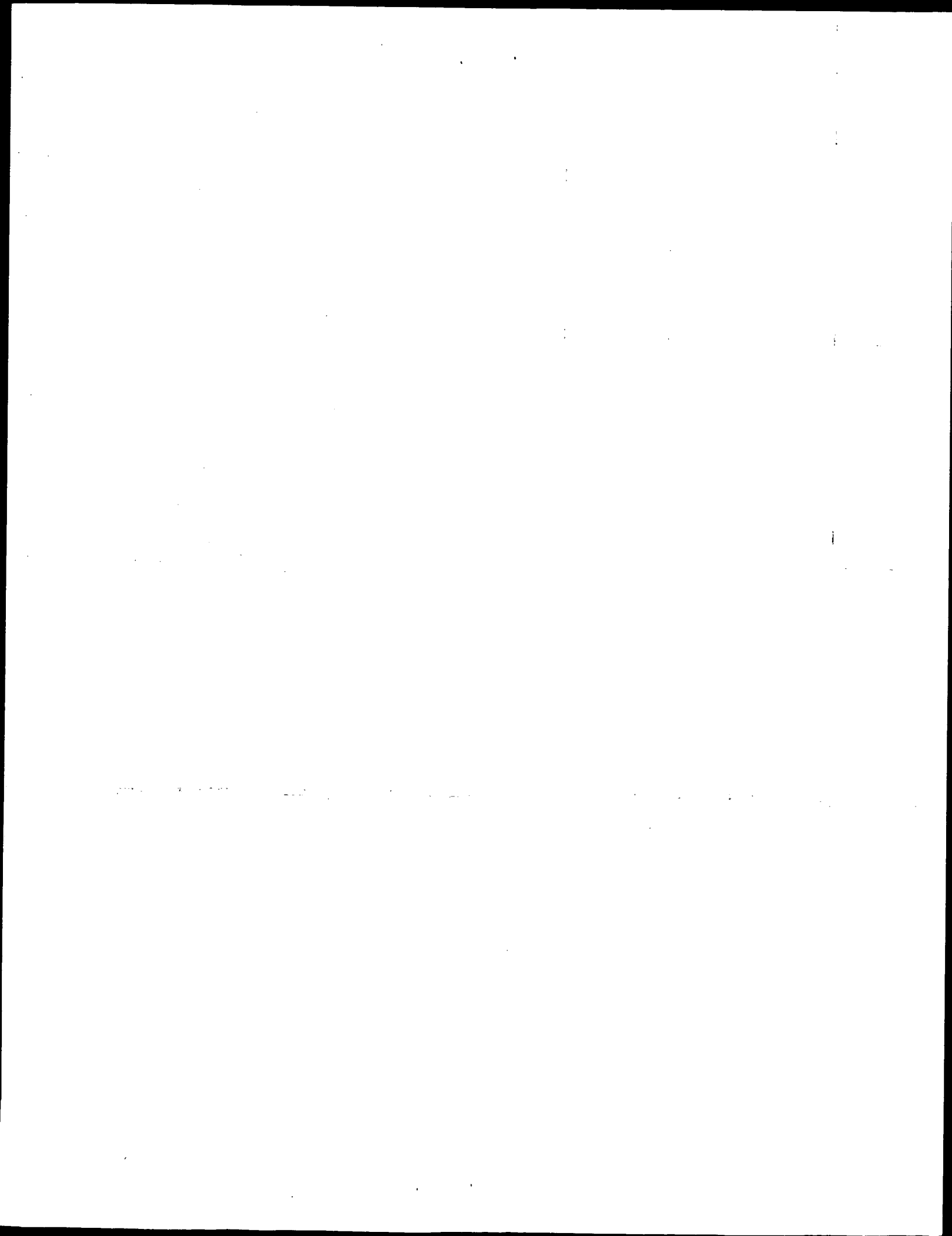
Statistics: Mean 7.011; Variance 3.159; scale 2.219

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	ID	Description	Pred. No.
No matches found.					

Search completed: Mon Aug 2 12:26:05 1999
Job time : 383 secs.



Release 3.1A John F. Collins, Biocomputing Research Unit
Copyright (c) 1993-1998 University of Edinburgh, U.K.
Distribution rights by Oxford Molecular Ltd

MPSrch_nn	n.a.	-	n.a.	database search, using Smith-Waterman algorithm
-----------	------	---	------	---

```
Run on: Mon Aug 2 12:32:12 1999; MasPar time 33.71 Seconds
165 378 Million cell updates/sec
```

Tabular output not generated.

Title: >US-09-121-239-27

```

Description: (1 20) .....
Perfect Score: 26

```

N.A.	sequence:	1
Comp:	GTGAGTCGGTGACCTAAATTCGTCTC	

Scoring table: TABLE default

८
७
६
५
४
३
२
१

MIHALCH SID : DBASE V, QUERY 0

searched: 2/17/00 seqs, 10/1/000000000000

```

post-processing: Minimum Match of
Listing first 1000 summa

```

n-gene:55
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part32 33:part33
34:part34 35:part35 36:part36 37:part37 38:part38
39:part39 40:part40 41:part41 42:part42 43:part43
44:part44 45:part45 46:part46 47:part47 48:part48
49:part49 50:part50 51:part51 52:part52 53:part53
54:part54 55:part55 56:part56 57:part57 58:part58
59:part59 60:part60

Statistics: Mean 5.552; Variance 3.164; scale 1.755

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No
1	21	80.8	40	45	V39474	Chronic myelogenous 1	1.70e-02
2	18	69.2	18	45	V39476	Chronic myelogenous 1	8.55e-01
3	18	69.2	18	3	D21921	3'-random oligomer to	1.12e+01
4	16	51.5	39	6	G37185	Ribozyme gene insert	1.12e+01
5	15	57.7	40	10	G37149	Chromosomal transloc	3.77e+01
6	14	53.8	18	45	V39477	Chronic myelogenous 1	1.23e+02
7	14	53.8	30	6	G37186	Bcr-abl mRNA sequence	1.23e+02
8	14	53.8	31	40	V01787	Antisense RNA sequenc	1.23e+02

C	9	1.3	50.0	17.1	N814569	Probe to B-cell diffe	3.86e+02
C	10	1.3	50.0	17.10	O56374	Sequence of Probe No.	3.86e+02
C	11	1.3	50.0	18.9	bcr mRNA ribozyme cle	3.86e+02	3.86e+02
C	12	1.5	50.0	22.6	O34636	Human bcr exon 3 5' p	3.86e+02
C	13	1.5	50.0	30.40	V01786	Antisense RNA sequenc	3.86e+02
C	14	1.3	50.0	40.40	V01604	Antisense RNA sequenc	3.86e+02
C	15	1.2	46.2	47.59	V97765	Human BgF-r target se	1.16e+03
C	16	1.2	46.2	21.8	O24837	MCPE 603 VL CDRI walk	1.16e+03
C	17	1.2	46.2	18.5	928817	HLA Class II gene loc	1.16e+03
C	18	1.2	46.2	28.12	O74572	Probe for the detecti	1.16e+03
C	19	1.2	46.2	28.12	O74497	Probe for the detecti	1.16e+03
C	20	1.2	46.2	28.15	O86609	Human immunodeficienc	1.16e+03
C	21	1.2	46.2	29.56	V92365	Human A-Raf hammethea	1.16e+03
C	22	1.2	46.2	33.3	O46735	HIV amplifier probe H	1.16e+03
C	23	1.2	46.2	33.17	O89511	Human immunodeficienc	1.16e+03
C	24	1.2	46.2	34.15	O86468	Primer, e24, for ampl	1.16e+03
C	25	1.2	46.2	36.4	O25115	PCR primer 21/M5.	1.16e+03
C	26	1.2	46.2	36.4	O25114	PCR primer 21/M5.	1.16e+03
C	27	1.2	46.2	39.2	O11445	Probe #8 complementar	1.16e+03
C	28	1.2	46.2	39.2	O11451	Probe #13 complementa	1.16e+03
C	29	1.2	46.2	46.8	O49401	HIV-1 TATA region.	1.16e+03
C	30	1.2	46.2	49.37	T755880	Competitor of 43 kDa	1.16e+03
C	31	1.2	46.2	50.25	O41198	Human T-cell lymphotr	1.16e+03
C	32	1.2	46.2	50.11	O89727	AIDS-associated retro	1.16e+03
C	33	1.2	46.2	50.11	O93726	Human T-cell lymphotr	1.16e+03
C	34	1.2	46.2	50.50	V95660	HIV-1 TATA region OLI	1.16e+03

Note: Post-processor removed 964 summaries from list due to search parameters chosen.

ALIGNMENTS

```

ID RESULT 1
AC V39474 standard; DNA: 40 BP.
AD V39474:
DT 22-SEP-1998 (first entry)
DE Chronic myelogenous leukaemia model target oligonucleotide.
KW Acute lymphocytic leukaemia; Chronic myelogenous leukaemia; ALL; CML;
KW target; capture probe; detection probe; hybridisation; bcr; abl;
KW multiple analyte; Salmonella; chromosomal translocation;
KW Philadelphia chromosome; ss.
OS Synthetic.
OS Homo sapiens.
PN EP-846776-42.
PN 10-JUN-1998.
PF 05-DEC-1997: 309831.
PF 06-DEC-1996; US-761131.
PA (VYSI-) VYSIS INC.
PI Lane DJ, Muller GR;
PI WPI: 98-299988/27.
PT Assay device for isolating analyte from sample, e.g. Salmonella in
PT food - comprises tube containing linear array of binding elements,
PT linked to binding factor to which component binds
PS Example 2; Page 12; 25pp; English.
PS An assay device has been developed for isolating an analyte from a
PS sample. The assay device comprises a tube containing a linear array of
PS binding elements, each linked to a distinct binding factor to which a
PS corresponding specific component binds. Where each of the binding
PS elements is configured to sealingly contact the interior surface of the
PS tube along the entire circumference of the binding element. The present
PS sequence represents a model target used in an example from the new
PS invention for the detection of chromosomal translocations. The new
PS sample and device can be used to detect e.g. Salmonella in a food
PS sample. They are also used to detect chromosomal translocations to
PS detect the 'Philadelphia' chromosome responsible for acute lymphocytic
PS leukaemia and chronic myelogenous leukaemia.
SO Sequence 40 BP; 10 A; 10 C; 8 G; 12 T;

Query Match 80.8%; Score 21; DB 45; Length 40;
Best Local Similarity 95.7%; Pred. No. 1; 70e-02;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

OY ||||| 2 ACTCAGCCACTGATTTAGAG 24

RESULT 2
ID V39476 standard; DNA; 18 BP.

AC Q21921;
DT 25-JUN-1992 (first entry)
DE Chronic myelogenous leukaemia capture probe.
KW Acute lymphocytic leukaemia; Chronic myelogenous leukaemia; ALL; CML; target; capture probe; detection probe; hybridisation; bcr; abl;
KW Philadelphia chromosome; ss.
OS Synthetic.

PN Homo sapiens.
EN EP-846776-A2.
PD 10-JUN-1998.
PF 05-DEC-1997; 309831.
PR 06-DEC-1996; US-761131.
PA (VYSI-) VYSIS INC.
PI Lane DJ, Muller UR;
DR WPI; 98-299988/27.

PT Assay device for isolating analyte from sample, e.g. Salmonella in food - comprises tube containing linear array of binding elements, linked to binding factor to which component binds
PS Example 2: Page 12: 25pp; English.

CC An assay device has been developed for isolating an analyte from a sample. The assay device comprises a tube containing a linear array of binding elements, each linked to a distinct binding factor to which a corresponding specific component binds, where each of the binding elements is configured to sealingly contact the interior surface of the tube along the entire circumference of the binding element. The present sequence represents a capture probe used in an example from the present invention for the detection of chromosomal translocations. The new method and device can be used to detect e.g. Salmonella in a food sample. They are also used to detect chromosomal translocations to detect the 'Philadelphia' chromosome responsible for acute lymphocytic leukemia and chronic myelogenous leukaemia.
CC Sequence 18 BP: 5 A; 3 C; 5 G; 5 T;

Query Match 69.2%; Score 18; DB 45; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.95e-01;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 taatccagtgcgtgagt 18
19 TAAATCCAGTGCCTGACT 2

RESULT 3
ID Q21921 standard; DNA; 18 BP.
AC Q21921;
DT 25-JUN-1992 (first entry)
DE 3'-tandem oligomer to disrupt bcr/abl junction secondary structure.
KW Philadelphia chromosome; CML; P210(abi/bcr) protein expression; antileukemia therapy; methylphosphonate oligonucleotide; ss.
OS Synthetic.

FT misc_feature 2..3
FT misc_feature 3..4
FT misc_feature 4..5
FT misc_feature 5..6

FT misc_feature 4..5
FT misc_feature 5..6
FT misc_feature 5..6
FT misc_feature 5..6

FT /note= "see comments"
FT 6..7
FT /tag= e
FT /label= non-phosphodiester_bond
FT /note= "see comments"

FT misc_feature 7..8
FT /tag= f
FT /label= non-phosphodiester_bond
FT /note= "see comments"

FT misc_feature 8..9
FT /tag= g
FT /label= non-phosphodiester_bond
FT /note= "see comments"

FT misc_feature 9..10
FT /tag= h
FT /label= non-phosphodiester_bond
FT /note= "see comments"

FT misc_feature 10..11
FT /tag= i
FT /label= non-phosphodiester_bond
FT /note= "see comments"

FT misc_feature 11..12
FT /tag= j
FT /label= non-phosphodiester_bond
FT /note= "see comments"

FT misc_feature 12..13
FT /tag= k
FT /label= non-phosphodiester_bond
FT /note= "see comments"

FT misc_feature 13..14
FT /tag= l
FT /label= non-phosphodiester_bond
FT /note= "see comments"

FT misc_feature 14..15
FT /tag= m
FT /label= non-phosphodiester_bond
FT /note= "see comments"

FT misc_feature 15..16
FT /tag= n
FT /label= non-phosphodiester_bond
FT /note= "see comments"

FT misc_feature 16..17
FT /tag= o
FT /label= non-phosphodiester_bond
FT /note= "see comments"

FT misc_feature 17..18
FT /tag= p
FT /label= non-phosphodiester_bond
FT /note= "see comments"

FT misc_feature 17..18
FT /tag= p
FT /label= non-phosphodiester_bond
FT /note= "see comments"

FT misc_feature 17..18
FT /tag= p
FT /label= non-phosphodiester_bond
FT /note= "see comments"

FT misc_feature 17..18
FT /tag= p
FT /label= non-phosphodiester_bond
FT /note= "see comments"

FT misc_feature 17..18
FT /tag= p
FT /label= non-phosphodiester_bond
FT /note= "see comments"

FT misc_feature 17..18
FT /tag= p
FT /label= non-phosphodiester_bond
FT /note= "see comments"

FT misc_feature 17..18
FT /tag= p
FT /label= non-phosphodiester_bond
FT /note= "see comments"

FT misc_feature 17..18
FT /tag= p
FT /label= non-phosphodiester_bond
FT /note= "see comments"

Query Match 69.2%; Score 18; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.95e-01;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 aaatccagtgcgtgagt 18
|||||

Cp 18 AATCCAGTGGCTGAGTG 1

RESULT 4

ID 037185 standard; DNA; 39 BP.

AC 13-NOV-1992 (first entry)

DE Ribozyme gene insert oligonucleotide (2).

DE Hammerhead; ribozyme; bcr-abl; catalytic domain; target; ss.

OS Synthetic.

PN W09303141-A.

PD 18-FEB-1993.

PF 01-AUG-1991; U05443.

PR 01-AUG-1991; WO-005443.

PA (CITY) CITY OF HOPE.

PI Forman SJ, Rossi JJ, Snyder DS;

DR WPI; 93-076498/09.

PR purging leukaemia cells from bone marrow - by ex vivo treatment

PT with a ribozyme that inhibits expression of Bcr-ABL gene prod.

PS "hammerhead" ribozyme to cleave bcr-abl mRNA was prep'd. The

CC disclosure; Page 9; 30pp; English.

CC A ribozyme contains a 22 nucleotide catalytic RNA sequence flanked by 15

CC nucleotide targeting sequences that position the catalytic domain at

CC the target site by Watson-Crick base pairing.

CC The double-stranded ribozyme gene insert with two flanking BamHI

CC restriction sites were prep'd. from two single-stranded

CC oligonucleotides (037184-85).

SQ Sequence 39 BP; 9 A; 10 C; 9 G; 11 T;

Query Match 61.5%; Score 16; DB 6; Length 39;

Best Local Similarity 100.0%; Pred. No. 1.12e+01;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 7 ctgacttaagcaag 22

11 CTGATTACCAAG 26

RESULT 5

ID 057149 standard; DNA; 40 BP.

AC 057149;

DE 26-JUL-1994 (first entry)

DE Chromosomal translocation detection probe #58.

KW Probe; detection; chromosomal translocation; leukemia; sarcoma;

KW lymphoma; chondrodysplasia; Prader-Willi syndrome; trisomy;

KW endocrine dysplasia; muscular hypotonia; incontinentia pigmenti;

KW rhabdo-myosarcoma; myelodysplasia; refractory anaemia;

KW balanced X-autosome; Beckwith-Wiedemann syndrome; ss.

OS Synthetic.

PN W09402500-A.

PD 03-FEB-1994.

PF 16-JUL-1993; U06674.

PR 17-JUL-1993; US-915900.

PA (AFRO-) APROGENEX INC.

PA (TEKA) UNIV TEXAS SYSTEM.

PI Asgari M, Blicik W, Bresser J, Cabbage ML, Ju SC;

DR WPI; 94-048785/06.

PT Oligonucleotides for detecting chromosomal translocations - with

PT sequence complementary to translocation junction-spanning nucleic

PT acid segment

PS Disclosure; Page 64; 75pp; English.

CC The sequences given in 057092-150 are probes which were used in the

CC detection of chromosomal translocations. These oligonucleotides

CC comprise a nucleotide sequence complementary to that of a

CC translocation junction-spanning cellular nucleic acid segment where

CC the translocation is inter- or intra-chromosomal. These probes may

CC also be used as primers for detecting chromosomal translocations

CC associated with diseases, esp. leukemia, sarcoma, lymphoma,

CC chondrodysplasia, Prader-Willi syndrome, muscular hypotonia,

CC incontinentia pigmenti, rhabdo-myosarcoma, trisomy, myelodysplasia,

CC refractory anaemia, balanced X-autosome, Beckwith-Wiedemann syndrome

CC or endocrine dysplasia.

SQ Sequence 40 BP; 9 A; 10 C; 9 G; 12 T;

Query Match 57.7%; Score 15; DB 10; Length 40;

Best Local Similarity 100.0%; Pred. No. 3.77e+01;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 26 ctctgccttaatcca 40

26 CTCTGCTTAATCCA 12

RESULT 6

ID V39477 standard; DNA; 18 BP.

AC V39477;

DE 22-SEP-1998 (first entry)

DE Chronic myelogenous leukaemia capture probe 2MS with mismatches.

KW Acute lymphocytic leukaemia; Chronic myelogenous leukaemia; ALL; CML;

KW target; capture probe; detection probe; hybridisation; bcr; abl;

KW Multiple analysis; Salmonella; chromosomal translocation;

KW Philadelphia chromosome; ss.

OS Synthetic.

PN Homo sapiens.

PD EP-846776-A2.

PF 10-JUN-1998.

PR 05-DEC-1997; 309831.

PA (VYSI-) VYSIS INC.

PI Lane DJ, Muller UR;

DR WPI; 98-299988/27.

PT Assay device for isolating analyte from sample, e.g. Salmonella in

PT food - comprises tube containing linear array of binding elements,

PT linked to binding factor to which component binds

PS Example 2; Page 12; 25pp; English.

CC An assay device has been developed for isolating an analyte from a

CC sample. The assay device comprises a tube containing a linear array of

CC binding elements, each linked to a distinct binding factor to which a

CC corresponding specific component binds, where each of the binding

CC elements is configured to sealingly contact the interior surface of the

CC tube along the entire circumference of the binding element. The present

CC sequence represents a capture probe used in an example from the present

CC invention for the detection of chromosomal translocations. The new

CC method and device can be used to detect e.g. Salmonella in a food

CC sample. They are also used to detect chromosomal translocations to

CC detect the Philadelphia chromosome responsible for acute lymphocytic

CC leukaemia and chronic myelogenous leukaemia.

SQ Sequence 18 BP; 5 A; 3 C; 5 G; 5 T;

Query Match 53.8%; Score 14; DB 45; Length 18;

Best Local Similarity 88.9%; Pred. No. 1.23e+02;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 1 taaatgcagtcctgagt 18

19 TAAATCAGTGGCTGAGT 2

RESULT 7

ID 037186 standard; mRNA; 30 BP.

AC 037186;

DE 13-NOV-1992 (first entry)

DE Bcr-abl mRNA sequence.

KW Hammerhead; ribozyme; bcr-abl; catalytic domain; target;

KW cell proliferation; Ph1+; Philadelphia chromosome;

KW chronic myelogenous leukemia; CML; acute lymphoblastic leukemia;

KW ALL; ss.

OS Synthetic.

PN Key

PD misc-feature

PF 19.20

PR /tag- a

PR /label- fusion_site

PR /tag- b

PR /note- "hammerhead" catalytic domain target"

PN W09303141-A.
 PD 18-FEB-1993.
 PF 01-AUG-1991; 005443.
 PR 01-AUG-1991; WO-005443.
 PA (CITY) CITY OF HOPE.
 PI Forman SJ, Rossi JJ, Snyder DS;
 DR WPI: 93-076498/09.
 PT purging leukaemia cells from bone marrow - by ex vivo treatment
 with a ribozyme that inhibits expression of BCR-ABL gene prod.
 PS Disclosure; Fig 1, 30pp; English.
 CC The ribozyme cleaves the bcr-abl mRNA specifically and can inhibit
 CC Ph1+ cell proliferation and/or differentiation. The ribozyme can
 CC be used to purge leukaemia cells from the bone marrow of patients
 CC with chronic myelogenous leukemia (CML) or acute lymphoblastic
 CC leukemia (ALL), esp. ex vivo. The purged bone marrow is then used
 CC to reconstitute the patients' haematopoietic system.
 SQ Sequence 30 BP; 10 A; 6 C; 7 G; 7 U;

Query Match 53.8%; Score 14; DB 6; Length 30;
 Best Local Similarity 78.6%; Pred. No. 1.23e+02;
 Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 1 ggaunuaagcagag 14
 |||:|||||
 QY 13 GGATTAACGACAG 26

RESULT 8
 ID V01787 standard; RNA; 31 BP.
 AC V01787;
 DT 04-JUN-1998 (first entry)
 DE Antisense RNA sequence of the specification.
 KW Antisense; inhibitor; gene expression; chromosomal translocation;
 KW translocation point; pharmaceutical composition;
 KW chronic myelogenous leukaemia; acute lymphoblastic leukaemia;
 KW acute myelogenous leukaemia; Non-Hodgkin lymphoma; treatment; ss.
 OS Synthetic.
 PN W09746672-A2.
 PD 11-DEC-1997.
 PF 05-JUN-1997; E02923.
 PR 05-JUN-1996; EP-109034.
 PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
 PI Haas R, Kronenwett R, Sczakiel G;
 DR WPI: 98-042181/04.
 PT Nucleic acid molecule containing chromosomal translocation point -
 PT useful to treat chromosomal translocation disorders, e.g. chronic
 PT myelogenous leukaemia
 PS Claim 6; Page 36; 49pp; English.
 CC V01779-804 represent antisense RNA sequences. For long chain antisense
 CC RNA, the association rate with their target RNA in vitro correlates
 CC with their effectiveness in vivo. Antisense molecules are potent
 CC inhibitors of gene expression and viral functions. The antisense
 CC molecules V01773-804 exemplify novel nucleic acid molecules of the
 CC invention. These nucleic acid molecules contain portions complementary to
 CC a first and second chromosomal DNA sequence. The nucleic acid molecule
 CC forms at least part of a chromosomal translocation resulting in a fusion
 CC gene containing the translocation point. The DNA sequence, as well as
 CC vectors and host cells containing it are useful in pharmaceutical
 CC compositions for treating disorders based on chromosomal translocations,
 CC preferably for chronic myelogenous leukaemia. The pharmaceutical
 CC composition may also be used to treat acute lymphoblastic leukaemias,
 CC acute myelogenous leukaemias and Non-Hodgkin lymphomas.
 SQ Sequence 31 BP; 7 A; 7 C; 7 G; 10 U;

Query Match 53.8%; Score 14; DB 40; Length 31;
 Best Local Similarity 64.3%; Pred. No. 1.23e+02;
 Matches 9; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Db 18 cucucuaaauac 31
 ||:|||||:|||||
 Cp 26 CTCGCTTAATCC 13

RESULT 9
 ID N81469 standard; DNA; 17 BP.
 AC N81469;
 DT 15-OCT-1990 (first entry)
 DE Probe to B-cell differentiation factor (BCDF) encoding gene.
 KW B-cell differentiation factor; BCDF; cancer; autoimmune.
 OS Homo sapiens.
 PN EP-257406-A.
 PD 2-MAR-1988.
 PF 6-AUG-1988; 111409.
 PR 06-AUG-1986; JP-184858.
 PR 27-AUG-1986; JP-200433.
 PR 18-DEC-1986; JP-302699.
 PR 13-MAY-1987; JP-116332.
 PA (AJIN) AJINOMOTO KK.
 PI Kishimoto TN, Hirano T, Matsui H, Takahara Y, Akiyama Y, Okano A;
 DR WPI: 88-057698/09.
 PT Purified polypeptide with B-cell differentiation factor activity -
 PT useful in prodn. of antibodies for diagnosis and therapy of
 PT cancers, infectious diseases etc.
 PS Example 3; Page 15-16; 72pp; English.
 CC Probe is used to generate peptide with BCDF activity, which
 CC may be used in the production and repair of B-cells. Also
 CC useful in treatment of autoimmune diseases, malignant tumors
 CC and may be used to influence B-cells to produce Abs in vitro.
 SQ Sequence 17 BP; 4 A; 3 C; 3 G; 2 T; 5 Others;

Query Match 50.0%; Score 13; DB 1; Length 17;
 Best Local Similarity 58.8%; Pred. No. 3.86e+02;
 Matches 10; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Db 1 gcycaaraaycargyt 17
 ||:|:|||||:|
 Cp 22 GCTTAATCCAGTGCT 6

RESULT 10
 ID Q56274 standard; DNA; 17 BP.
 AC Q56274;
 DT 15-SEP-1994 (first entry)
 DE Sequence of Probe No. 8-2 based on B-cell differentiation factor
 DE fragment (BCDF) no. 8.
 KW B-cell differentiation factor; BCDF; antitumour; antiviral;
 KW lymphokine; ss.
 OS Synthetic.
 PN EP-585957-A.
 PD 09-MAR-1994.
 PF 06-AUG-1987; 111409.
 PR 06-AUG-1986; JP-184858.
 PR 27-AUG-1986; JP-200433.
 PR 18-DEC-1986; JP-302699.
 PR 13-MAY-1987; JP-116332.
 PA (AJIN) AJINOMOTO KK.
 PI (KISH) KISHIMOTO T.
 PI Akiyama Y, Hirano T, Kishimoto T, Matsui H, Okano A;
 DR WPI: 94-076278/10.
 PT New non-glycosylated human B-cell differentiation factor -
 PT lacking signal sequence and produced in bacteria, useful as
 PT immuno therapeutic for stimulating antibody prodn, treating
 PT cancer etc, also DNA encoding it
 PS Example; Page 15; 63pp; English.
 CC Human T cells transformed by human T cell leukaemia virus (HTLV)
 CC produce BCDF. BCDF was prepd. from the supernatant of cultured
 CC VT-1 cells. The N-terminal sequence was determined to be:
 CC PVPGGNSKRVAA. The BCDF prepn. was digested with Lysyl
 CC endopeptidase. The resultant fragment 3 has the sequence:
 CC KSLAAE. The resultant fragment 8 has the sequence: KLXQNEWLGXM.
 CC Q56267-Q56274 show the sequences of mixtures of probes based
 CC on Fragment 3, Fragment 8 and the N-terminal AA sequence of
 CC BCDF.
 SQ Sequence 17 BP; 4 A; 3 C; 3 G; 2 T;

CC preferably for chronic myelogenous leukaemia. The pharmaceutical
 CC composition may also be used to treat acute lymphoblastic leukaemias,
 CC acute myelogenous leukaemia and Non-Hodgkin lymphomas.
 SQ Sequence 30 BP; 7 A; 6 C; 7 G; 10 U;

Query Match 50.0%; Score 13; DB 40; Length 30;
 Best Local Similarity 61.5%; Pred. No. 3.86e+02;
 Matches 8; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Db 18 cucugcuaaanc 30
 1:|||||:|
 Cp 26 CTCGCTTAATC 14

RESULT 14
 ID V01804 standard; RNA; 40 BP.
 AC V01804;
 DT 04-JUN-1998 (first entry)
 DE Antisense RNA sequence of the specification.
 KW Translocation point; gene expression; chromosomal translocation;
 KW Translocation point; pharmaceutical composition;
 KW chronic myelogenous leukaemia; acute lymphoblastic leukaemia;
 KW acute myelogenous leukaemia; Non-Hodgkin lymphoma; treatment; ss.
 OS Synthetic.
 PN WO9746672-A2.
 PD 11-DEC-1997.
 PF 05-JUN-1997; E02923.
 PR 05-JUN-1996; EP-109034.
 PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
 PI Haas R, Kronenwett R, Szakiel G;
 DR WPI; 98-042181/04.
 PT Nucleic acid molecule containing chromosomal translocation point -
 PT useful to treat chromosomal translocation disorders, e.g. chronic
 PT myelogenous leukaemia
 PS Claim 6; Page 37; 49pp; English.
 CC V01779-804 represent antisense RNA sequences. For long chain antisense
 CC RNA, the association rate with their target RNA in vitro correlates
 CC with their effectiveness in vivo. Antisense molecules are potent
 CC inhibitors of gene expression and viral functions. The antisense
 CC molecules V01779-804 exemplify novel nucleic acid molecules of the
 CC invention. These nucleic acid molecules contain portions complementary to
 CC a first and second chromosomal DNA sequence. The nucleic acid molecule
 CC forms at least part of a chromosomal translocation resulting in a fusion
 CC gene containing the translocation point. The DNA sequence, as well as
 CC vectors and host cells containing it are useful in pharmaceutical
 CC compositions for treating disorders based on chromosomal translocations,
 CC preferably for chronic myelogenous leukaemia. The pharmaceutical
 CC composition may also be used to treat acute lymphoblastic leukaemias,
 CC acute myelogenous leukaemias and Non-Hodgkin lymphomas.
 SQ Sequence 40 BP; 8 A; 10 C; 10 G; 12 U;

Query Match 50.0%; Score 13; DB 40; Length 40;
 Best Local Similarity 61.5%; Pred. No. 3.86e+02;
 Matches 8; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Db 28 cucugcuaaanc 40
 1:|||||:|
 Cp 26 CTCGCTTAATC 14

RESULT 15
 ID V97763 standard; RNA; 17 BP.
 AC V97763;
 DT 17-MAR-1999 (first entry)
 DE Human EGF-R target sequence nucleotide position 4299.
 KW Human; epidermal growth factor receptor; EGFR; EGF-R; target sequence;
 KW hammerhead ribozyme; hairpin ribozyme; inhibition; cell proliferation;
 KW cancer; genetic drift; detection; mutation; ss.
 OS Homo sapiens.
 PN WO9833893-A2.
 PD 06-AUG-1998.
 PF 14-JAN-1998; U00730.
 PR 04-DEC-1997; US-985162.

PR 31-JAN-1997; US-036476.
 PA (RIBO-) RIBOZYME PHARM INC.
 PA (UYAS-) UNIV ASTON.
 PI Akhtar S, Fell P, McSwiggen JA;
 DR WPI; 98-437449/37.
 PT Enzymatic nucleic acids - which cleave RNA derived from an epidermal
 PT growth factor receptor, useful for inhibiting cell proliferation and
 PT for treating cancers
 PS Claim 5; Page 79; 109pp; English.
 CC The present invention describes enzymatic nucleic acid molecules (NAMS)
 CC which specifically cleave RNA derived from an epidermal growth factor
 CC receptor (EGF-R) gene. V97221 to V98043 and V98979 to V99090 represent
 CC specifically claimed target sequence from human EGF-R. V98044 to V98866
 CC and V98867 to V9878 represent hammerhead ribozymes and hairpin ribozymes
 CC respectively for human EGF-R. The NAMS are useful for cleaving EGF-R RNA
 CC in the treatment of a condition associated with EGF-R expression levels
 CC e.g. to inhibit cell proliferation in the prevention or treatment of
 CC cancers. The NAMS can also be used as diagnostic tools to examine
 CC genetic drift and mutations within diseased cells or to detect the
 CC presence of EGF-R RNA in a cell.
 SQ Sequence 17 BP; 2 A; 3 C; 5 G; 7 U;

Query Match 46.2%; Score 12; DB 59; Length 17;
 Best Local Similarity 56.3%; Pred. No. 1.16e+03;
 Matches 9; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Db 1 ucguuauuacagag 16
 1:|||||:|
 Cp 23 TCCTTAATCACTG 8

RESULT 16
 ID Q14330 standard; DNA; 18 BP.
 AC Q14330;
 DT 15-JAN-1992 (first entry)
 DE MCPC 603 VL CDR1 walk-through mutagenesis oligonucleotide (Ser, His).
 KW Mutagenesis; monoclonal antibody; Fv molecule; ss.
 OS Synthetic.
 PN WO9115581-A.
 PD 17-OCT-1991.
 PF 05-APR-1991; U02362.
 PR 05-APR-1990; US-505314.
 PA (CREA/) CREA R.
 PI Crea R;
 DR WPI; 91-325224/44.
 PT Walk-through mutagenesis of proteins - by introducing predetermined
 PT amino acid in each sequence position in preselected region of the
 PT protein
 PS Disclosure, Fig 8A; 91pp; English.
 CC Walk-through mutagenesis of five out of six CDRs of the MCPC 603 Fv
 CC molecule is performed, and Asp, His and Ser are the preselected amino
 CC acids. In this model, walk-through mutagenesis is carried out from two
 CC to three times with a different amino acid in a given region or domain.
 CC For example, Ser and His are sequentially walked-through VL CDR1, and
 CC Asp and Ser are sequentially walked-through VL CDR3 (Q14331).
 CC VL CDR2 was not targeted for mutagenesis because structural studies
 CC indicated that this region contributes little to the binding site in
 CC MCPC 603. In CDR1 of the VH chain of the Fv, Asp and His are walked
 CC through (Q14332). Ser can be introduced at two positions in CDR1
 CC with a single base change. In VH CDR2, His and Ser are the
 CC preselected amino acids used (Q14333) and in VH CDR3, Asp, His and
 CC Ser are each walked through the amino terminal five positions of
 CC CDR3 (Q14334).
 CC See also Q14321-34.
 SQ Sequence 18 BP; 0 A; 3 C; 1 G; 2 T;

Query Match 46.2%; Score 12; DB 3; Length 18;
 Best Local Similarity 28.6%; Pred. No. 1.16e+03;
 Matches 4; Conservative 9; Mismatches 1; Indels 0; Gaps 0;

Db 5 mkmkryhccgtsht 18
 1:|||||:|
 Gy 3 CTCACCCACTGAT 16


```
RESULT 17
ID Q28817 standard: DNA: 21 BP.
AC Q28817:
DE 26-FEB-1993 (first entry)
DE HLA Class II gene locus PCR primer DOB6.
DE Polymerase chain reaction: MHC genotype: human leukocyte antigen;
KW major histocompatibility complex; automated determination: ss.
OS Synthetic.
PN W0215711-A.
PF 17-SEP-1992.
PF 04-MAR-1992: U01675.
PR 18-FEB-1992: US-665960.
PR 18-FEB-1992: US-833668.
PA (MINU) UNIV MINNESOTA.
PI Barbosa JJ, Boyce-Jacino MT, Farns AJ, Rich SS, Santamaria P;
PI WPI: 92-331755/40.
DR Fully automated determ. of MHC genotype - by isolating nucleic
PT acid from sample, amplifying nucleic acid by PCR to sequence
PT alleles and analysing sequenced prods.
PS Example: Page 22: 105pp: English.
CC The sequence is that of a PCR primer used as part of a method for
CC determining the major histocompatibility complex (MHC) genotype of
CC a subject in a sample. The primer anneals to nucleotides -8/-2 of
CC HLA class II locus DOB1.
CC See also Q28761-Q28800 and Q28811-Q28819.
SQ Sequence 21 BP; 4 A; 7 C; 7 G; 3 T;

Query Match 46.2%; Score 12; DB 5; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.16e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 10 ccagtgctgag 21
CP 14 CCAGTGCTGAG 3

RESULT 18
ID Q74572 standard: RNA: 28 BP.
AC Q74572:
DE 05-MAY-1995 (first entry)
DE Probe for the detection of HIV-1.
DE Probe: primer; detection: amplification; identification; diagnosis;
KW HIV-1; human immunodeficiency virus; HTLV-1; AIDS;
KW human T-cell leukaemia virus; acquired immune deficiency syndrome;
KW ss.
OS Synthetic.
PN EP-617132-A.
PF 28-SEP-1994.
PF 28-MAR-1994: 302196.
PR 26-MAR-1993: US-040745.
PA (GENP-) GEN-PROBE INC.
PI McDonough SH, Ryder TB, Yang Y;
PI WPI: 94-295780/37.
DR New oligonucleotides corresponding to HIV-1 sequences - used for
PT selective amplification and as hybridisation probes for detection
PT of HIV-1.
PS Claim 1: Page 51: 69pp: English.
CC Probes and primers specific for HIV-1 were identified by comparison
CC of published sequences of HIV-1, HIV-2, HTLV-1 and HTLV-2 and were
CC then synthesised. The probes are able to detect HIV-1 in a sample
CC and distinguish it from its known closest phylogenetic neighbours.
CC See Q74533-Q74574.
SQ Sequence 28 BP; 7 A; 10 C; 5 G; 6 U;

Query Match 46.2%; Score 12; DB 12; Length 28;
Best Local Similarity 59.1%; Pred. No. 1.16e+03;
Matches 13; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
```

```
RESULT 19
ID Q74497 standard: DNA: 28 BP.
AC Q74497:
DE 04-MAY-1995 (first entry)
DE Probe for the detection of HIV-1.
DE Probe: primer; detection: amplification; identification; diagnosis;
KW HIV-1; human immunodeficiency virus; HTLV-1; AIDS;
KW human T-cell leukaemia virus; acquired immune deficiency syndrome;
KW ss.
OS Synthetic.
PN EP-617132-A.
PF 28-SEP-1994.
PF 28-MAR-1994: 302196.
PR 26-MAR-1993: US-040745.
PA (GENP-) GEN-PROBE INC.
PI McDonough SH, Ryder TB, Yang Y;
PI WPI: 94-295780/37.
DR New oligonucleotides corresponding to HIV-1 sequences - used for
PT selective amplification and as hybridisation probes for detection
PT of HIV-1.
PS Claim 1: Page 3: 69pp: English.
CC Probes and primers specific for HIV-1 were identified by comparison
CC of published sequences of HIV-1, HIV-2, HTLV-1 and HTLV-2 and were
CC then synthesised. The probes are able to detect HIV-1 in a sample
CC and distinguish it from its known closest phylogenetic neighbours.
CC See Q74486-Q74499.
SQ Sequence 28 BP; 6 A; 5 C; 10 G; 7 T;

Query Match 46.2%; Score 12; DB 12; Length 28;
Best Local Similarity 77.3%; Pred. No. 1.16e+03;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

DB 5 ctgctatgcgagctcgtgag 26
CP 24 CTGCTATGCAGCTCGTGCAG 3

RESULT 20
ID Q86609 standard: DNA: 28 BP.
AC Q86609:
DE 15-NOV-1995 (first entry)
DE Human immunodeficiency virus (HIV) region 1 probe.
DE Primer; autocatalytic; target; HIV; ss.
OS Synthetic.
PN US5399491-A.
PF 21-MAR-1995.
PF 11-JUL-1989: 379501.
PR 10-JUL-1990: US-550837.
PR 19-MAR-1992: US-855732.
PA (GENP-) GEN-PROBE INC.
PI Fultz TJ, Kacian DL;
PI WPI: 95-130686/17.
DR Amplification of nucleic acid targets - using a reverse
PT transcriptase with RNase H activity and a RNA polymerase at
PT constant temp.
PS Disclosure: Column 9: 58pp: English.
CC Q86607-09 are primers and a probe for the human immunodeficiency
CC virus region 1. They are used to produce autocatalytic
CC oligonucleotides which require no change in the experimental
CC conditions i.e. constant temperature, pH and ionic strength.
CC These sequences are useful in generating multiple copies of
CC specific nucleic acid target sequences.
SQ Sequence 28 BP; 6 A; 5 C; 10 G; 7 T;

Query Match 46.2%; Score 12; DB 15; Length 28;
Best Local Similarity 77.3%; Pred. No. 1.16e+03;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

CP 24 CTCGTTAAATCAGTGGCTGAG 3

RESULT 21
 ID V92356 standard; RNA: 29 BP.
 DE V92356;
 DT 18-FEB-1999 (first entry)
 DE Human A-Raf hammerhead ribozyme position 2347.
 DE Human: c-raf; A-raf; B-raf; hammerhead ribozyme; hairpin ribozyme;
 KW target; substrate; catalyst; modulation; expression; Raf gene;
 KW delivery; screening; identification; synthesis; deprotection;
 KW purification; cancer; inflammation; psoriasis; non-hepatic ascites;
 KW infection; genetic drift; restenosis; rheumatoid arthritis; ss.
 OS Synthetic.
 OS Homo sapiens.
 PN W09850530-A2.
 PD 12-NOV-1998.
 PF 05-MAY-1998: 009249.
 PR 19-DEC-1997: US-068212.
 PR 09-MAY-1997: US-046059.
 PR 09-JUN-1997: US-049002.
 PR 03-JUL-1997: US-051718.
 PR 22-AUG-1997: US-056808.
 PR 02-OCT-1997: US-061321.
 PR 02-OCT-1997: US-061324.
 PR 05-NOV-1997: US-064866.
 PA (RIBO-) RIBOZYME PHARM INC.
 PI Beaudry A, Beigelman L, Bellon L, Jarvis T,
 PI Karpeisky A, Kislich K, Matulic-Adamic J, McSwigen JA,
 PI Parry T, Reynolds M, Sweedler D, Thompson J, Workman CT;
 DR: WPI: 99-009494/01.
 PT Identifying new catalytic nucleic acid that modulates selected
 PT processes - especially ribozymes that cleave Raf RNA for treating
 PT cancer, restenosis, and also new ribozymes and modified nucleoside
 PT triphosphates used as antiviral agents and synthons
 CC Claim 151: Page 162; 259pp: English.
 CC A method has been developed for the identification of a nucleic acid
 CC capable of modulating a process in a biological system. The method
 CC comprises: (a) introducing into the system a random library of nucleic
 CC acid catalysts (NAC) having a substrate binding domain (SBD), comprising
 CC a random sequence, and a catalytic domain (CD); and (b) identifying NAC
 CC in systems where modulation has occurred and/or determining the sequence
 CC of at least part of the SBDs in such systems. Nucleic acid molecules with
 CC endonuclease activity and catalytic activity, from the present invention,
 CC are used to modulate gene expression in plant and mammalian cells and to
 CC cleave target nucleic acid, particularly for treating systemic diseases
 CC caused by specific RNA, e.g. cancer, inflammation, psoriasis, non-hepatic
 CC ascites and infection. They may also be used to detect genetic drift and
 CC mutations in diseased cells and to determine c-raf RNA. Specifically NACs
 CC with RNA-cleaving activity that modulate expression of the Raf gene, are
 CC used to treat cancer, restenosis, psoriasis or rheumatoid arthritis, or
 CC generally any condition associated with the level of c-raf. Introducing
 CC of sugar/phosphate modifications increases stability against nuclease
 CC and activity. V90922 to V93877 represent NACs that can be used in the
 CC method, specifically for modulating the expression of a Raf gene.
 SQ Sequence 29 BP: 8 A; 6 C; 9 G; 5 U;
 Query Match 46.2%; Score 12; DB 56; Length 29;
 Best Local Similarity 75.0%; Pred. No. 1.16e+03;
 Matches 9; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 Db 1 uccagugcuga 12
 Cp 15 TCCAGTGGCTGA 4
 RESULT 22
 ID Q46735 standard; DNA: 33 BP.
 AC Q46735;
 DT 16-DEC-1993 (first entry)
 DE HIV amplifier probe HIV.151.
 KW Probe; hybridisation; assay; detection;
 KW human immunodeficiency virus; HIV; human lymphotropic retrovirus;

KW solution phase; comb-type branched polynucleotide; sidechain;
 KW extension; binding site; ligation; template; linker; ss.
 OS Synthetic.
 PN W09315223-A.
 PD 08-JUL-1993.
 PF 22-DEC-1992: U11168.
 PR 23-DEC-1991: US-813583.
 PA (CHIR) CHIRON CORP.
 PI Irvine BD, Kolberg JA, Urdea MS;
 DR: WPI: 93-227337/28.
 PT Synthetic oligo/nucleotide useful as amplifier probe for HIV
 PT detection - comprises 1st segment complementary to HIV sequence
 PT and 2nd segment complementary to oligo unit of nucleic acid
 PT multimer
 PS Claim 1; Page 73; 92pp: English.
 CC A "15 x 3" amplified soln. phase nucleic acid sandwich hybridisation
 CC assay employs two multimers: (1) an amplifier probe having a first
 CC segment (A) that binds to HIV and a second segment (B) that
 CC hybridises to (2) an amplifier multimer having a first segment (B*)
 CC that hybridises to the segment (B) and fifteen iterations of a
 CC segment (C), wherein segment C hybridises to three labeled
 CC oligonucleotides.
 CC HIV amplifier probes are given in Q46703-742.
 CC HIV capture probes are given in Q46743-752.
 CC Each amplifier probe contained, in addition to the sequences
 CC complementary to the HIV sequences, the 5' extension given in
 CC Q46753, complementary to a segment of the amplifier multimer.
 CC Each capture probe contained, in addition to the sequences given
 CC complementary to the HIV sequences, a downstream sequence given
 CC in Q46734, complementary to the DNA bound to the solid phase.
 CC In addition to the amplifier and capture probes, a set of HIV
 CC spacer oligonucleotides (Q46755-61) was included in the
 CC hybridisation mixt.
 SQ Sequence 33 BP: 7 A; 11 C; 3 G; 7 T;
 Query Match 46.2%; Score 12; DB 7; Length 33;
 Best Local Similarity 64.3%; Pred. No. 1.16e+03;
 Matches 9; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Db 14 ctgtrathcchg 27
 Cp 24 CTCGTTAAATCAG 11
 RESULT 23
 ID Q89511 standard; cDNA: 33 BP.
 AC Q89511;
 DT 04-DEC-1995 (first entry)
 DE Human immunodeficiency virus (HIV) probe.
 KW Human immunodeficiency virus; HIV; probe; nucleotide; hybridisation;
 KW ss.
 OS Synthetic.
 PN USH001431-H.
 PD 04-APR-1995.
 PF 04-NOV-1992: 971719.
 PR 04-NOV-1992: US-971719.
 PA (KERN/) KERN D G.
 PA (SHER/) SHERIDAN P J.
 PA (TODD/) TODD J.
 PI Kern DG, Sheridan PJ, Todd J;
 DR: WPI: 95-146201/19.
 PT Facilitating sepn. of pellet and supernatant in centrifuged sample -
 PT in nucleotide hybridisation assays, by adding beads to the sample to
 PT assist identification of the pellet area, improves precision
 PS Example 1: Column 8: 17pp: English.
 CC Q89479-Q89518 are HIV specific labelled probes which can be used in
 CC a nucleotide hybridisation assay (NHA). The assay demonstrates a new
 CC method using "beads" in sample preparation which increases the
 CC precision of NHAs.
 SQ Sequence 33 BP: 7 A; 11 C; 3 G; 7 T;
 Query Match 46.2%; Score 12; DB 15; Length 33;
 Best Local Similarity 64.3%; Pred. No. 1.16e+03;

Matches 9; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
 Db 14 ccyttrathchg 27
 |||:|:|:|:|:|
 Cp 24 CTCGTTAAATCCAG 11

RESULT 24
 ID 086488 standard; cDNA; 34 BP.
 AC 086488:
 DT 24-NOV-1995 (first entry)
 DE Primer: e24, for amplification of E2F-1 DNA binding region.
 KM Primer: E2F-1, E2F-2, transcription; factor; retinoblastoma; pRb;
 KW tumour; suppressor; ss.
 OS Synthetic.
 PN GB2282814-A.
 PD 19-APR-1995.
 PF 07-OCT-1994; 020283.
 PR 13-OCT-1993; US-136119.
 PA (MERI) MERCK & CO INC.
 PI Heimbrook DC, Ivey-Hoyle M, Oloff AI;
 DR WPI: 95-141220/19.
 PT New human transcription factor E2F-2 - involved in cell cycle
 regulation and useful for drug screening; also related cDNA,
 PT plasmids and transformed cells.
 PS Example 1; Page 15; 53pp; English.
 CC 086484-91 correspond to the E2F-1 primers e20-27 and fl20
 CC respectively. The amplified E2F-1 DNA binding region is
 CC substantially complementary to the E2F-2 coding region and is
 CC used as a probe for this region. E2F-2 is involved in cell cycle
 CC regulation in particular binding of E2F to the retinoblastoma
 CC gene product (pRb) causes down regulation of the transcription
 CC of any genes containing the E2F binding site. E2F-2 is useful in
 CC the study of cell cycle regulation especially in the study
 CC of pRb and certain viral oncogenes and oncoproteins.
 SQ Sequence 34 BP; 6 A; 7 C; 11 G; 10 T;

Query Match 46.2%; Score 12; DB 15; Length 34;
 Best Local Similarity 100.0%; Pred. No. 1.16e+03;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 12 cagccactgat 23
 |||:|:|:|:|:|
 Qy 5 CAGCCACTGAT 16

RESULT 25
 ID 025115 standard; DNA; 36 BP.
 AC 025115:
 DT 23-NOV-1992 (first entry)
 DE PCR primer 21/M6.
 KM TNF; tumour necrosis factor; murein; P75; P55; receptor;
 KW amplification; polymerase chain reaction; ss.
 OS Synthetic.
 PN Key
 FT mutation Location/Qualifiers
 FT 7,9
 FT /*tag= a
 FT mutation 11..12
 FT /*tag= b
 PN EP-486908-A.
 PD 27-MAY-1992.
 PF 11-NOV-1991; 119128.
 PR 21-NOV-1990; EP-810901.
 PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
 PI Fiers W, Tavernier J, Van Ostadex;
 DR WPI: 92-176547/22.
 PT Human tumour necrosis factor mutants - show difference in binding
 PT affinity to P75 and P55 TNF receptors, for treatment of tumours
 PS Example 7; Page 18; 38pp; English.
 CC The oligomer sequence corresponds to the complement of nucleotides
 CC 219-184 of the TNF plasmid pBS56/RBStII-SplI-TNF-alpha (mutated
 CC bases are given in the features table). The primer 21/M6 was used
 CC in one of three PCR reactions to generate mutant forms of TNF-alpha

CC e.g. Glu31-TNF and Asn31-Thr32-TNF. The mutants displays a difference
 CC in binding affinity to P75 and P55 TNF receptors and are useful in
 CC pharmaceutical compns. in conjunction with non-toxic carrier
 CC molecules for the treatment of e.g. cancer.
 CC See also Q25113-9.
 SQ Sequence 36 BP; 5 A; 11 C; 10 G; 10 T;

Query Match 46.2%; Score 12; DB 4; Length 36;
 Best Local Similarity 100.0%; Pred. No. 1.16e+03;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 15 tcagccactgga 26
 |||:|:|:|:|:|
 Qy 4 TCAGCCACTGGA 15

RESULT 26
 ID 025114 standard; DNA; 36 BP.
 AC 025114:
 DT 23-NOV-1992 (first entry)
 DE PCR primer 21/M6.
 KM TNF; tumour necrosis factor; murein; P75; P55; receptor;
 KW amplification; polymerase chain reaction; ss.
 OS Synthetic.
 PN Key
 FT mutation Location/Qualifiers
 FT 10..12
 FT /*tag= a
 FT /*note= "mutation site"
 PN EP-486908-A.
 PD 27-MAY-1992.
 PF 11-NOV-1991; 119128.
 PR 21-NOV-1990; EP-810901.
 PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
 PI Fiers W, Tavernier J, Van Ostadex;
 DR WPI: 92-176547/22.
 PT Human tumour necrosis factor mutants - show difference in binding
 PT affinity to P75 and P55 TNF receptors, for treatment of tumours
 PS Example 7; Page 18; 38pp; English.
 CC The oligomer sequence corresponds to the complement of nucleotides
 CC 219-184 of the TNF plasmid pBS56/RBStII-SplI-TNF-alpha. The primer
 CC 21/M6 was used in one of three PCR reactions to generate mutant forms
 CC of TNF-alpha e.g. Glu31-TNF and Asn31-Thr32-TNF. The mutants display
 CC a difference in binding affinity to P75 and P55 TNF receptors and are
 CC useful in pharmaceutical compns. in conjunction with non-toxic carrier
 CC molecules for the treatment of e.g. cancer.
 CC See also Q25113-9.
 SQ Sequence 36 BP; 4 A; 15 C; 9 G; 8 T;

Query Match 46.2%; Score 12; DB 4; Length 36;
 Best Local Similarity 100.0%; Pred. No. 1.16e+03;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 15 tcagccactgga 26
 |||:|:|:|:|:|
 Qy 4 TCAGCCACTGGA 15

RESULT 27
 ID 011446 standard; DNA; 39 BP.
 AC 011446:
 DT 29-MAY-1991 (first entry)
 DE Probe #8 complementary to CD1a target sequence contg. AT or TA.
 KM CD1a; gene inhibition; inflammation; neoplasm; ss.
 OS Synthetic.
 PN J03007585-A.
 PD 14-JAN-1991.
 PF 21-SEP-1989; 410622.
 PR 23-JAN-1989; US-299265.
 PR 21-SEP-1989; US-410622.
 PA (UYVA-) YALE UNIV.
 DR WPI: 91-08455/13.
 PT Selective inhibition of gene manifestation - with optically active
 PT oligonucleotide reacting with target DNA to inhibit cell functions

PS Claim 4; Page 2; 19pp; Japanese.
CC This oligonucleotide is one of 14 that are complementary to regions
CC of the CD4 coding sequence and have an AT or TA motif within
CC nucleotides 12-20. The oligonucleotides are used in pharmaceutical
CC compositions with a UV-radiated optically active compound such as a
CC psoralen. The UV-radiated product is able to react with target DNA
CC under optically active conditions to inhibit cell functions.
CC See also Q11435-Q11445 and Q11447-Q11456, Q11544-7.
SQ Sequence 39 BP; 10 A; 10 C; 9 G; 10 T;

Query Match 46.2%; Score 12; DB 2; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.16e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 25 cagccactgcat 36
|||||
QY 5 CAGCCACTGAT 16

RESULT 28
ID Q11451 standard; DNA; 39 BP.
AC Q11451;
DT 29-MAY-1991 (first entry)
DE Probe #13 complementary to CD4 target sequence contg. AT or TA.
KW CD4; gene inhibition; inflammation; neoplasm; ss.
OS Synthetic.
PN J03007585-A.
PD 14-JAN-1991.
PF 21-SEP-1989; 410622.
PR 23-JAN-1989; US-299265.
PE 21-SEP-1989; US-410622.
PA (UYRA-) YALE UNIV.
DR WPI; 91-089455/13.
PT Selective inhibition of gene manifestation - with optically active
PT oligonucleotide reacting with target DNA to inhibit cell functions
PS Claim 4; Page 2; 19pp; Japanese.
CC This oligonucleotide is one of 14 that are complementary to regions
CC of the CD4 coding sequence and have an AT or TA motif within
CC nucleotides 12-20. The oligonucleotides are used in pharmaceutical
CC compositions with a UV-radiated optically active compound such as a
CC psoralen. The UV-radiated product is able to react with target DNA
CC under optically active conditions to inhibit cell functions.
CC See also Q11435-Q11450 and Q11452-Q11465, Q11544-7.
SQ Sequence 39 BP; 11 A; 10 C; 7 G; 11 T;

Query Match 46.2%; Score 12; DB 2; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.16e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 8 cagccactgcat 19
|||||
QY 5 CAGCCACTGAT 16

RESULT 29
ID Q49401 standard; CDNA; 46 BP.
AC Q49401;
DT 27-APR-1994 (first entry)
DE HIV-1 TATA region.
KW TATA modulating factor; TMF; transcription; TATA box; promoter; HIV-1;
KW human immunodeficiency virus-1; short arm; human chromosome 3; p12-p21;
KW translocation; cancer; ss.
OS Human immunodeficiency virus-1.
PN W09320106-A.
PD 14-OCT-1993.
PE 31-MAR-1993; U03077.
PR 02-APR-1992; US-862025.
PA (TEXA) UNIV TEXAS SYSTEM.
PI Gaynor RB, Wu F;
DR WPI; 93-336836/42.
PT New protein cellular factor - capable of binding double stranded
PT HIV-1 tata region and activating gene expression of HIV-LTR
PS Claim 3; Page 48; 75pp; English.

CC This sequence represents the TATA region of the HIV-1 LTR from -46
CC to -1. This region is bound by TATA modulating factor (TMF). TMF
CC is a protein of mol. wt. 123-130 kD which activates transcription in
CC most genes, esp. in human immunodeficiency virus-1 (HIV-1) by binding
CC to the TATA box region of the promoter. TMF is encoded by the short
CC arm of human chromosome 3 in the region p12-p21 which is often
CC involved in translocations in patients having lung and other types
CC of cancer.
SQ Sequence 46 BP; 8 A; 12 C; 11 G; 15 T;

Query Match 46.2%; Score 12; DB 8; Length 46;
Best Local Similarity 77.3%; Pred. No. 1.16e+03;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;







Db 7 ctcaagatgcatataagcag 28
|||||
QY 3 CTCAGCCACTGATTTAGCAG 24

RESULT 30
ID T95880 standard; DNA; 49 BP.
AC T95880;
DT 27-MAR-1998 (first entry)
DE Competitor of 43 kDa TAR DNA binding protein (TDP-43).
KW Tat-activation; TAR region; DNA binding protein; TDP-43;
KW human immunodeficiency virus type-1; HIV-1; long terminal repeat;
KW LTR; inhibition; gene expression; treatment; infection;
KW competitor; ss.
OS Human immunodeficiency virus type 1.
PN U5568511-A.
PD 18-NOV-1997.
PE 22-NOV-1994; 343682.
PR 05-NOV-1994; US-343682.
PR 05-NOV-1991; US-788266.
PR 06-MAY-1994; US-239047.
PA (TEXA) UNIV TEXAS SYSTEM.
PI Gaynor RB, Ou ST, Wu FK;
DR WPI; 98-007932/01.
PT Polypeptide(s) that inhibit HIV-1 gene expression - useful for
PT treating AIDS
PS Example 8; Columns 51-52; 31pp; English.
CC The present sequence is a competitor of the 43 kDa
CC Tat-activation (TAR) DNA binding protein (TDP-43), which binds a
CC TAR region of human immunodeficiency virus type-1 (HIV-1) long
CC terminal repeat (LTR) DNA, does not bind to TAR RNA and inhibits
CC HIV-1 gene expression. TDP-43 can be used to treat HIV-1
CC infections.
SQ Sequence 49 BP; 9 A; 13 C; 12 G; 15 T;

Query Match 46.2%; Score 12; DB 37; Length 49;
Best Local Similarity 77.3%; Pred. No. 1.16e+03;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Db 7 ctcaagatgcatataagcag 28
|||||
QY 3 CTCAGCCACTGATTTAGCAG 24

Search completed: Mon Aug 2 12:34:47 1999
Job time : 155 secs.

MPSrch_nn	n.a.	-	n.a.	database search, using Smith-Waterman algorithm
-----------	------	---	------	---

```
Run on:      Mon Aug 2 12:22:01 1999;      MasPar time 7.16 Seconds
Tabular output not generated.              257.475 Million cell updates/sec
```

Title:	>US-09-121-239-27
Description:	(1-26) from US09121239.seq
Perfect Score:	26
N.A. Sequence:	1 CACTCAGCCACATGATTTAAGCAGAG 26
Comp:	GTGAGTCGGTGACCTTAATTCGCTC

Scoring table: TABLE default

Nmāтч STD : Dbase 0; Query 0

```
Searched:      137068 seqs, 35432894 bases
Post-processing: Minimum Match 08
                  Listing first 1000 summaries
                  Maximum DB seq length 50
```

Database:

```
n-issued
1:5A_COMB 2:5B_COMB 3:5C_COMB 4:PCT9_COMB 5:backfiles1
```

Statistics: Mean 5.211; Variance 2.655; scale 1.963

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
c	1	21	80.8	40	3	US-08-761	Sequence 2, Applicatio	5.79e+00
c	2	18	69.2	18	3	US-08-761	Sequence 4, Applicatio	5.28e+00
c	3	14	53.8	18	3	US-08-761	Sequence 5, Applicatio	1.47e+00
c	4	13	50.0	18	2	US-08-761	Sequence 9, Applicatio	5.45e+00
c	5	13	50.0	22	4	PCT-US22-0	Sequence 12, Applicati	5.45e+00
c	6	13	50.0	22	2	US-08-152	Sequence 12, Applicati	5.45e+00
c	7	12	46.2	20	2	US-08-152	Sequence 46, Applicati	1.93e+00
c	8	12	46.2	21	1	US-07-165	Sequence 47, Applicati	1.93e+00
c	9	12	46.2	21	1	US-08-106	Sequence 47, Applicati	1.93e+00
c	10	12	46.2	23	1	US-08-106	Sequence 98, Applicati	1.93e+00
c	11	12	46.2	28	2	US-08-799	Sequence 64, Applicati	1.93e+00
c	12	12	46.2	28	2	US-08-799	Sequence 92, Applicati	1.93e+00
c	13	12	46.2	28	2	US-08-799	Sequence 78, Applicati	1.93e+00
c	14	12	46.2	28	2	US-08-799	Sequence 12, Applicati	1.93e+00
c	15	12	46.2	34	1	US-08-336	Sequence 9, Applicatio	1.93e+00
c	16	12	46.2	35	2	US-08-443	Sequence 12, Applicati	1.93e+00
c	17	12	46.2	36	1	US-07-794	Sequence 23, Applicati	1.93e+00
c	18	12	46.2	36	1	US-08-041	Sequence 13, Applicati	1.93e+00
c	19	12	46.2	36	1	US-08-041	Sequence 12, Applicati	1.93e+00

[illegible]

```

CC Patent No. 5804384
CC GENERAL INFORMATION:
CC APPLICANT: M Iler, Uwe R. et al.
CC TITLE OF INVENTION: DEVICES AND METHODS FOR DETECTING
CC TITLE OF INVENTION: MULTIPLE ANALYTES IN SAMPLES
CC NUMBER OF SEQUENCES: 7
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Vysis, Inc.
CC STREET: 3100 Woodcreek Drive
CC CITY: Downers Grove
CC STATE: Illinois
CC COUNTRY: U.S.A.
CC ZIP: 60515
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Diskette
CC APPLICATION NUMBER: US/08/761,131
CC FILING DATE:
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER:
CC FILING DATE:
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Galloway, No. 5804384val B.
CC REGISTRATION NUMBER: 33,595
CC REFERENCE/DOCKET NUMBER: 01886/064001
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 708-271-7417
CC TELEFAX: 708-271-7048
CC TELEX: 200154
CC INFORMATION FOR SEQ ID NO: 2:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 40 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: genomic DNA
CC SEQUENCE 40 BP; 10 A; 10 C; 12 T; 0 OTHER.
CC
CC Query Match 80.8%; Score 21; DB 3; Length 40;
CC Best Local Similarity 95.7%; Pred. No. 5,79e-04;
CC Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0.
CC
CC Db 1 ACTCAGCCACTGGATTAAAGTAG 23
CC ||||||||||||||||
CC 0Y 2 ACTCAGCCACTGGATTAAAGCAG 24
CC
CC RESULT 2
CC ID US-08-761-131-4 STANDARD; DNA; UNC; 18 BP.
CC AC xxxxxx
CC DT
CC DE Sequence 4, Application US/08761131
CC CC Sequence 4, Application US/08761131
CC CC Patent No. 5804384
CC CC GENERAL INFORMATION:
CC CC APPLICANT: M Iler, Uwe R. et al.
CC CC TITLE OF INVENTION: DEVICES AND METHODS FOR DETECTING
CC CC TITLE OF INVENTION: MULTIPLE ANALYTES IN SAMPLES
CC CC NUMBER OF SEQUENCES: 7
CC CC CORRESPONDENCE ADDRESS:
CC CC ADDRESSEE: Vysis, Inc.
CC CC STREET: 3100 Woodcreek Drive
CC CC CITY: Downers Grove
CC CC STATE: Illinois
CC CC COUNTRY: U.S.A.
CC CC ZIP: 60515
CC CC COMPUTER READABLE FORM:
CC CC MEDIUM TYPE: Diskette
CC CC COMPUTER: IBM Compatible

```

```
CC OPERATING SYSTEM: DOS
CC SOFTWARE: FastSeq Version 2.0
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/761,131
CC FILING DATE:
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER:
CC FILING DATE:
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Galloway, No. 5804384val B.
CC REGISTRATION NUMBER: 33,595
CC REFERENCE/DOCKET NUMBER: 01886/064001
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 708-271-7417
CC TELEFAX: 708-271-7048
CC TELEX: 200154
CC INFORMATION FOR SEQ ID NO: 4:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 18 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: Genomic DNA
CC SEQUENCE 18 BP; 5 A; 5 C; 5 G; 5 T; 0 OTHER.
SQ
Query Match 69.2%; Score 18; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.28e-02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 TAAATCAGTGGCTGAGT 18
19 TAAATCAGTGGCTGAGT 2

RESULT 3
ID US-08-761-131-5 STANDARD; DNA; UNC; 18 BP.
AC xxxxxx
DE Sequence 5, Application US/08761131
Sequence 5, Application US/08761131
Patent No. 5804384
GENERAL INFORMATION:
CC APPLICANT: M Iler, Uwe R. et al.
CC TITLE OF INVENTION: DEVICES AND METHODS FOR DETECTING
CC TITLE OF INVENTION: MULTIPLE ANALYTES IN SAMPLES
CC NUMBER OF SEQUENCES: 7
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Vysis, Inc.
CC STREET: 3100 Woodcreek Drive
CC CITY: Downers Grove
CC STATE: Illinois
CC COUNTRY: U.S.A.
CC ZIP: 60515
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Diskette
CC COMPUTER: IBM Compatible
CC OPERATING SYSTEM: DOS
CC SOFTWARE: FastSeq Version 2.0
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/761,131
CC FILING DATE:
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER:
CC FILING DATE:
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Galloway, No. 5804384val B.
CC REGISTRATION NUMBER: 33,595
CC REFERENCE/DOCKET NUMBER: 01886/064001
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 708-271-7417
CC TELEFAX: 708-271-7048
CC
```

CC TELEX: 200154
CC INFORMATION FOR SEQ ID NO: 5:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 18 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: Genomic DNA
CC SEQUENCE 18 BP; 5 A; 3 C; 5 G; 5 T; 0 OTHER.
SQ
Query Match 53.8%; Score 14; DB 3; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.47e+01;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Db 1 TAAATGAGTGCCTGACT 18
Cp 19 TAAATCAGTGCCTGACT 2
RESULT 4
ID US-08-363-233B-9 STANDARD; DNA; UNC; 18 BP.
AC xxxxxx
DE Sequence 9, Application US/08363233B
CC Patent No. 5714383
CC GENERAL INFORMATION:
CC APPLICANT: Thompson, James D.
CC TITLE OF INVENTION: METHOD AND REAGENT FOR TREATING CHRONIC
CC NUMBER OF SEQUENCES: 39
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Lyon & Lyon
CC STREET: 633 West Fifth Street
CC CITY: Los Angeles
CC STATE: California
CC COUNTRY: U.S.A.
CC ZIP: 90071-2066
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
CC OPERATING SYSTEM: IBM P.C. DOS 5.0
CC SOFTWARE: FASTSEQ for Windows 2.0
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/363,233B
CC FILING DATE: December 23, 1994
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC PRIOR APPLICATION DATA: including application
CC PRIOR APPLICATION NUMBER: 07/882,822
CC APPLICATION NUMBER: 07/882,822
CC FILING DATE: May 14, 1992
CC APPLICATION NUMBER: 08/193,922
CC FILING DATE: February 7, 1994
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Walbury, Richard I.
CC REGISTRATION NUMBER: 32,327
CC REFERENCE/DOCKET NUMBER: 209/165
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (213) 469-1600
CC TELEFAX: (213) 955-0440
CC TELEX: 67-3510
CC INFORMATION FOR SEQ ID NO: 9:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 18 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
SQ SEQUENCE 18 BP; 7 A; 2 C; 4 G; 0 T; 5 OTHER.
Query Match 50.0%; Score 13; DB 2; Length 18;

Best Local Similarity 76.9%; Pred. No. 5.45e-01;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
Db 1 GAUUNAGCAGAG 13
Cy 14 GATTTAGCAGAG 26
RESULT 5
ID PCT-US92-05035-12 STANDARD; DNA; UNC; 22 BP.
AC xxxxxx
DE Sequence 12, Application PC/TUS9205035
CC Sequence 12, Application PC/TUS9205035
CC GENERAL INFORMATION:
CC APPLICANT: Calabretta, Bruno
CC APPLICANT: Gewirtz, Alan M.
CC TITLE OF INVENTION: Selective Inhibition of
CC TITLE OF INVENTION: Leukemic Cell Proliferation by bcr-abl
CC NUMBER OF SEQUENCES: 34
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Temple University - Of The Common-
CC STREET: 406 University Services Building
CC CITY: Philadelphia
CC STATE: Pennsylvania
CC COUNTRY: U.S.A.
CC ZIP: 19122
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
CC OPERATING SYSTEM: MS-DOS
CC SOFTWARE: Wordperfect 5.1
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US92/05035
CC FILING DATE: 19920615
CC CLASSIFICATION: 514
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 07/718,302
CC FILING DATE: June 18, 1991
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 07/869,911
CC FILING DATE: April 14, 1991
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Monaco, Daniel A.
CC REGISTRATION NUMBER: 30,480
CC REFERENCE/DOCKET NUMBER: 6056-120 (CIP) 1
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (215) 568-8383
CC TELEFAX: (215) 568-5549
CC TELEX: None
CC INFORMATION FOR SEQ ID NO: 12:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 22 Nucleotides
CC TYPE: NUCLEIC ACID
CC STRANDEDNESS: single stranded
CC TOPOLOGY: not relevant
SQ SEQUENCE 22 BP; 4 A; 9 C; 4 G; 5 T; 0 OTHER.
Query Match 50.0%; Score 13; DB 4; Length 22;
Best Local Similarity 100.0%; Pred. No. 5.45e+01;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 10 CACTGAGCACTG 22
Cy 1 CACTGAGCACTG 13
RESULT 6
ID US-08-152-621-12 STANDARD; DNA; UNC; 22 BP.
AC xxxxxx
DE

DE Sequence 12, Application US/08152621
CC Sequence 12, Application US/08152621
CC Patent No. 5652222
CC GENERAL INFORMATION:
CC APPLICANT: Calabretta, Bruno
CC APPLICANT: Gewirtz, Alan M.
CC TITLE OF INVENTION: Selective Inhibition of
CC TITLE OF INVENTION: Leukemic Cell Proliferation by bcr-abl
CC TITLE OF INVENTION: Antisense Oligonucleotides
CC NUMBER OF SEQUENCES: 34
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: SEIDEL, GONDA, LAVORGNA
CC ADDRESSEE: 4 MONACO, P.C.
CC STREET: 1800 Two Penn Center
CC CITY: Philadelphia
CC STATE: Pennsylvania
CC COUNTRY: U.S.A.
CC ZIP: 19102
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Diskette, 3.50 inch, 720 KB
CC COMPUTER: IBM PS/2
CC OPERATING SYSTEM: MS-DOS
CC SOFTWARE: WordPerfect 5.1
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/152,621
CC FILING DATE: No. 565222member 15, 1993.
CC CLASSIFICATION: 514
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 07/718,302
CC FILING DATE: June 18, 1991
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Monaco, Daniel A.
CC REGISTRATION NUMBER: 30,480
CC REFERENCE/DOCKET NUMBER: 6056-120 (CT.) 1
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (215) 568-8383
CC TELEFAX: (215) 568-5549
CC TELEX: No. 5652222e
CC INFORMATION FOR SEQ ID NO: 12:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 22 Nucleotides
CC TYPE: nucleic acid
CC STRANDEDNESS: single stranded
CC TOPOLOGY: not relevant
SQ SEQUENCE 22 BP; 4 A; 9 C; 4 G; 5 T; 0 OTHER.
Query Match 50.0%; Score 13; DB 2; Length 22;
Best Local Similarity 100.0%; Pred. No. 5.45e+01;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 10 CACTGAGCCACTG 22
QY 1 CACTGAGCCACTG 13
RESULT 7
ID US-08-259-745A-46 STANDARD; DNA; UNC; 20 BP.
AC xxxxxx
DE Sequence 46, Application US/08259745A
CC Sequence 46, Application US/08259745A
CC Patent No. 5582983
CC GENERAL INFORMATION:
CC APPLICANT: Anderson, Donald
CC APPLICANT: Scholin, Christopher
CC TITLE OF INVENTION: GENETIC MARKERS AND METHODS OF IDENTIFYING ALEXANDRIUM
CC NUMBER OF SEQUENCES: 49
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
CC STREET: 130 Water Street
CC CITY: Boston
CC STATE: MA
CC COUNTRY: U.S.A.

CC ZIP: 02109
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Diskette
CC COMPUTER: IBM Compatible
CC OPERATING SYSTEM: DOS
CC SOFTWARE: FastSeq Version 1.5
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/259,745A
CC FILING DATE: 14-JUN-1994
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 07/967,637
CC FILING DATE: 28-OCT-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Neuner, George W
CC REGISTRATION NUMBER: 26,964
CC REFERENCE/DOCKET NUMBER: 42,101 FWC
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 617-523-3400
CC TELEFAX: 617-523-6440
CC TELEX:
CC INFORMATION FOR SEQ ID NO: 46:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 20 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: preRNA
CC HYPOTHETICAL: NO
CC ANTI-SENSE: NO
CC FRAGMENT TYPE:
CC ORIGINAL SOURCE:
SQ SEQUENCE 20 BP; 7 A; 5 C; 3 G; 5 T; 0 OTHER.

Query Match 46.2%; Score 12; DB 1; Length 20;
Best Local Similarity 87.5%; Pred. No. 1.93e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
DB 3 CCGCTGATTTAAGCA 18
QY 8 CCAGTGATTTAAGCA 23

RESULT 8
ID US-07-665-960A-47 STANDARD; DNA; UNC; 21 BP.
AC xxxxxx
DE Sequence 47, Application US/07665960A
CC Sequence 47, Application US/07665960A
CC Patent No. 5578443
CC GENERAL INFORMATION:
CC APPLICANT: Santamaria, Pedro
CC APPLICANT: Boyce-Jacino, Michael T.
CC APPLICANT: Barbosa, Jose J.
CC APPLICANT: Rich, Stephen S.
CC APPLICANT: Faras, Anthony J.
CC TITLE OF INVENTION: DNA Sequence-Based HLA Typing
CC NUMBER OF SEQUENCES: 49
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Merchant & Gould
CC STREET: 3100 No. 5578443west Center
CC CITY: Minneapolis
CC STATE: Minnesota
CC COUNTRY: USA
CC ZIP: 55402
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Diskette, 3.5 inch, 720 KB.
CC COMPUTER: No. 5578443thgate 386
CC OPERATING SYSTEM: DOS 4.0
CC SOFTWARE: WordPerfect-5.0
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/07/665,960A

Mon Aug 2 13:59:02 1999

US-09-121-239-27.rml

Page 5

CC FILING DATE: 19910306
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Kowalchuk, Alan W.
CC REGISTRATION NUMBER: 31,535
CC REFERENCE/DOCKET NUMBER: 600.190-US-01
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (612) 332-5300
CC TELEFAX: (612) 332-9081
CC INFORMATION FOR SEQ ID NO: 47:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 21 base pairs
CC TYPE: NUCLEIC ACID
CC STRANDEDNESS: Single
CC TOPOLOGY: Linear
CC MOLECULE TYPE: Genomic DNA
CC ANTI-SENSE: no
CC FRAGMENT TYPE: Internal Fragment
CC ORIGINAL SOURCE: Synthetically Derived
CC FEATURE:
CC NAME/KEY: Oligonucleotide primer DOB6
CC LOCATION: Anneals to codons -8 to -2 of the
CC LOCATION: DOB1 transcript of HLA class II
SQ SEQUENCE 21 BP; 4 A; 7 C; 7 G; 3 T; 0 OTHER.

Query Match 46.2%; Score 12; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.93e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 10 CCAGTGGCTGAG 21
|||||
Cp 14 CCAGTGGCTGAG 3

RESULT 9
ID US-08-106-802-47 STANDARD; DNA; UNC; 21 BP.
AC xxxxxx
DE Sequence 47, Application US/08106802
CC Sequence 47, Application US/08106802
CC Patent No. 5629149
CC GENERAL INFORMATION:
CC APPLICANT: Santamaria, Pedro
CC APPLICANT: Boyce-Jacino, Michael T.
CC APPLICANT: Barbosa, Jose J.
CC APPLICANT: Rich, Stephen S.
CC APPLICANT: Farias, Anthony J.
CC TITLE OF INVENTION: DNA Sequence-Based HLA Typing
CC TITLE OF INVENTION: Method
CC NUMBER OF SEQUENCES: 49
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Merchant & Gould
CC STREET: 3100 No. 5629149west Center
CC CITY: Minneapolis
CC STATE: Minnesota
CC COUNTRY: USA
CC ZIP: 55402
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Diskette, 3.5 inch, 720 Kb.
CC COMPUTER: PC/XT/AT or compatible
CC OPERATING SYSTEM: MS-DOS 3.30
CC SOFTWARE: ASCII
CC SOFTWARE: (Origin: WordPerfect 5.0)
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/106,802
CC FILING DATE: 16-AUG-1993
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 07/833,668
CC FILING DATE: 18-FEB-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Kowalchuk, Alan W.
CC REGISTRATION NUMBER: 31,535

CC REFERENCE/DOCKET NUMBER: 600.243-US-01
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (612) 332-5300
CC TELEFAX: (612) 332-9081
CC INFORMATION FOR SEQ ID NO: 47:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 21 base pairs
CC TYPE: Nucleic Acid
CC STRANDEDNESS: Single
CC TOPOLOGY: Linear
CC MOLECULE TYPE: Genomic DNA
CC ANTI-SENSE: no
CC FRAGMENT TYPE: Internal Fragment
CC ORIGINAL SOURCE: Synthetically Derived
CC FEATURE:
CC NAME/KEY: Oligonucleotide primer DOB6
CC LOCATION: Anneals to codons -8 to -2 of the
CC LOCATION: DOB1 transcript of HLA class II
SQ SEQUENCE 21 BP; 4 A; 7 C; 7 G; 3 T; 0 OTHER.

Query Match 46.2%; Score 12; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.93e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 10 CCAGTGGCTGAG 21
|||||
Cp 14 CCAGTGGCTGAG 3

RESULT 10
ID US-08-399-412A-38 STANDARD; DNA; UNC; 23 BP.
AC xxxxxx
DE Sequence 98, Application US/08399412A
CC Sequence 98, Application US/08399412A
CC Patent No. 5622828
CC GENERAL INFORMATION:
CC APPLICANT: Palma, David
CC APPLICANT: Gold, Larry
CC TITLE OF INVENTION: High-Affinity Oligonucleotide
CC TITLE OF INVENTION: Ligands To Secretory Phospholipase
CC TITLE OF INVENTION: A2 (SPLA2)
CC NUMBER OF SEQUENCES: 122
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Swanson & Bratschun, L.L.C.
CC STREET: 8100 E. Prentice Avenue, Suite 200
CC CITY: Englewood
CC STATE: Colorado
CC COUNTRY: USA
CC ZIP: 80111
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB storage
CC COMPUTER: IBM compatible
CC OPERATING SYSTEM: MS-DOS
CC SOFTWARE: WordPerfect 5.1
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/399,412A
CC FILING DATE: 6-MARCH-1995
CC CLASSIFICATION: 536
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 07/714,131
CC FILING DATE: 10-JUNE-1991
CC CLASSIFICATION: 536
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 07/536,428
CC FILING DATE: 11-JUNE-1990
CC APPLICATION NUMBER: 07/964,624
CC FILING DATE: 21-OCTOBER-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Julie L. Beirard
CC REGISTRATION NUMBER: 36,450
CC REFERENCE/DOCKET NUMBER: NEX27

```
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: (303) 793-3333  
CC TELEFAX: (303) 793-3433  
CC INFORMATION FOR SEQ ID NO: 98:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 23 base pairs  
CC TYPE: nucleic acid  
CC STRANDEDNESS: single  
CC TOPOLOGY: linear  
CC SEQUENCE 23 BP; 3 A; 5 C; 4 G; 0 T; 11 OTHER.  
  
Query Match          46.2%; Score 12; DB 1; Length 23;  
Best Local Similarity 25.0%; Pred.No.1,93e+02;  
Matches      4; Conservative     10; Mismatches    2; Indels      0; Gaps      0.  
  
Cc      1 CUWRCUUCACRGYNAV 16  
       ||::||::||::|  
Cp      26 CTCCTGCTTAATTCAG 11  
  
RESULT   11  
ID US-08-479-852-64 STANDARD; DNA; UNC; 28 BP.  
AC xxxxxx  
DT  
DE Sequence 64, Application US/08479852  
CC Sequence 64, Application US/08479852  
CC Patent No. 5712385  
CC GENERAL INFORMATION:  
CC APPLICANT: Sherrol H. McDonough, Thomas B. Ryder,  
CC APPLICANT: Yeasing Yang  
CC TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION  
CC TITLE OF INVENTION: OLIGONUCLEOTIDES AND PROBES  
CC TITLE OF INVENTION: NO HUMAN IMMUNODEFICIENCY VIRUS TYPE 1  
CC NUMBER OF SEQUENCES: 139  
CC CORRESPONDENCE ADDRESSES:  
CC ADDRESSEE: Lyon & Lyon  
CC STREET: 611 West Sixth Street  
CC CITY: Los Angeles  
CC STATE: California  
CC COUNTRY: USA  
CC ZIP: 90017  
  
COMPUTER READABLE FORM:  
CC MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
CC COMPUTER: IBM PS/2 Model 502 or 55SX  
CC OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)  
CC SOFTWARE: WordPerfect (Version 5.0)  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/479, 852  
CC FILING DATE:  
CC CLASSIFICATION: 435  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/040, 745  
CC FILING DATE:  
CC APPLICATION NUMBER: U.S. Serial No. 5712385 07/550, 837  
CC FILING DATE: 7/10/90  
CC APPLICATION NUMBER: U.S. Serial No. 5712385 07/379, 501  
CC FILING DATE: 7/11/89  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Walburg, Richard J.  
CC REGISTRATION NUMBER: 32,327  
CC REFERENCE/DOCKET NUMBER: 196/189  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: (213) 489-1600  
CC TELEFAX: (213) 955-0440  
CC TELEX: 67-3510  
CC INFORMATION FOR SEQ ID NO: 64:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 28  
CC TYPE: nucleic acid  
CC STRANDEDNESS: single  
CC TOPOLOGY: linear  
CC SEQUENCE 28 BP; 7 A; 10 C; 5 G; 6 T; 0 OTHER.
```

Query Match	46.2%	Score 12:	DB 2:	Length 28:
Best Local Similarity	77.3%	Pred. No.	1.93e+02:	
Matches	17:	Conservative	0:	Mismatches 5; Indels 0; Gaps 0
DB	3	CTCAGATCTGCTATATAGCAG	24	
QY	3	CTCAGCCACTGATTTAGCAG	24	
RESULT	12			
ID	US-08-479-852-92	STANDARD;	DNA;	UNC; 28 BP.
AC	xxxxxx			
DT				
DE	Sequence 92, Application US/08479852			
CC	Sequence 92, Application US/08479852			
CC	Patent No. 5712385			
CC	GENERAL INFORMATION:			
CC	APPLICANT: Sherrol H. McDonough, Thomas B. Ryder,			
CC	APPLICANT: Yeasing Yang			
CC	TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION			
CC	TITLE OF INVENTION: OLIGONUCLEOTIDES AND PROBES			
CC	TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS TYPE 1			
CC	NUMBER OF SEQUENCES: 139			
CC	CORRESPONDENCE ADDRESS:			
CC	ADDRESSEE: Lyon & Lyon			
CC	STREET: 611 West Sixth Street			
CC	CITY: Los Angeles			
CC	STATE: California			
CC	COUNTRY: USA			
CC	ZIP: 90017			
CC	COMPUTER READABLE FORM:			
CC	MEDIUM TYP: 3.5" Diskette, 1.44 Mb storage			
CC	COMPUTER: IBM PS/2 Model 50Z or 555X			
CC	OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)			
CC	SOFTWARE: WordPerfect (Version 5.0)			
CC	CURRENT APPLICATION DATA:			
CC	APPLICATION NUMBER: US/08/479,852			
CC	FILING DATE:			
CC	CLASSIFICATION: 435			
CC	PRIOR APPLICATION DATA:			
CC	APPLICATION NUMBER: US/08/040,745			
CC	FILING DATE:			
CC	APPLICATION NUMBER: U.S. Serial No. 5712385			
CC	FILING DATE: 7/10/90			
CC	APPLICATION NUMBER: U.S. Serial No. 5712385			
CC	FILING DATE: 7/11/89			
CC	ATTORNEY/AGENT INFORMATION:			
CC	NAME: Warburg, Richard J.			
CC	REGISTRATION NUMBER: 32,327			
CC	REFERENCE/DOCKET NUMBER: 196/189			
CC	TELECOMMUNICATION INFORMATION:			
CC	TELEPHONE: (213) 489-1600			
CC	TELEFAX: (213) 955-0440			
CC	TELEX: 67-3510			
CC	INFORMATION FOR SEQ ID NO: 92:			
CC	SEQUENCE CHARACTERISTICS:			
CC	LENGTH: 28			
CC	TYPE: nucleic acid			
CC	STRANDEDNESS: single			
CC	TOPOLOGY: linear			
CC	SEQUENCE 28 BP; 7 A; 10 C; 5 G; 0 T; 6 OTHER.			
QY	Query Match	46.2%	Score 12:	DB 2; Length 28;
	Best Local Similarity	59.1%	Pred. No.	1.93e+02;
	Matches	13;	Conservative	4; Mismatches 5; Indels 0; Gaps 0;
DB	3	CTCAGATCTGCTATATAGCAG	24	
QY	3	CTCAGCCACTGATTTAGCAG	24	
RESULT	13			
ID	US-08-479-852-78	STANDARD;	DNA;	UNC; 28 BP.

AC xxxxxx
DE Sequence 78, Application US/08479852
CC Sequence 78, Application US/08479852
CC Patent No. 5712385
CC GENERAL INFORMATION:
CC APPLICANT: Sheriell H. McDonough, Thomas B. Ryder,
CC APPLICANT: Yeasing Yang
CC TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION
CC TITLE OF INVENTION: OLIGONUCLEOTIDES AND PROBES
CC NUMBER OF INVENTIONS: TO HUMAN IMMUNODEFICIENCY VIRUS TYPE 1
CC NUMBER OF SEQUENCES: 139
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Lyon & Lyon
CC STREET: 611 West Sixth Street
CC CITY: Los Angeles
CC STATE: California
CC COUNTRY: USA
CC ZIP: 90017
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
CC COMPUTER: IBM PS/2 Model 502 or 55SX
CC OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
CC SOFTWARE: WordPerfect (Version 5.0)
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/479,852
CC FILING DATE:
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US/08/040,745
CC FILING DATE:
CC APPLICATION NUMBER: U.S. Serial No. 5712385 07/550,837
CC FILING DATE: 7/10/90
CC APPLICATION NUMBER: U.S. Serial No. 5712385 07/379,501
CC FILING DATE: 7/11/89
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Kaitburg, Richard J.
CC REGISTRATION NUMBER: 32,327
CC REFERENCE/DOCKET NUMBER: 196/189
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (213) 489-1600
CC TELEFAX: (213) 955-0440
CC TELEX: 67-3510
CC INFORMATION FOR SEQ ID NO: 78:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 28
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC SEQUENCE 28 BP: 6 A; 5 C; 10 G; 0 T; 7 OTHER.
SQ
Query Match 46.2% Score 12; DB 2; Length 28;
Best Local Similarity 54.5% Pred. No. 1.93e+02;
Matches 12; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
Db 5 CTGCTTAATTCAGTGGCTGAG 26
Cp 24 CTGCTTAATTCAGTGGCTGAG 3
RESULT 14
ID US-08-479-852-12 STANDARD; DNA; UNC; 28 BP.
AC xxxxxx
DE Sequence 12, Application US/08479852
CC Sequence 12, Application US/08479852
CC Patent No. 5712385
CC GENERAL INFORMATION:
CC APPLICANT: Sheriell H. McDonough, Thomas B. Ryder,
CC APPLICANT: Yeasing Yang
CC TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION
CC TITLE OF INVENTION: OLIGONUCLEOTIDES AND PROBES
CC NUMBER OF INVENTIONS: TO HUMAN IMMUNODEFICIENCY VIRUS TYPE 1
CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS TYPE 1

CC NUMBER OF SEQUENCES: 139
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Lyon & Lyon
CC STREET: 611 West Sixth Street
CC CITY: Los Angeles
CC STATE: California
CC COUNTRY: USA
CC ZIP: 90017
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
CC COMPUTER: IBM PS/2 Model 502 or 55SX
CC OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
CC SOFTWARE: WordPerfect (Version 5.0)
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/479,852
CC FILING DATE:
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US/08/040,745
CC FILING DATE:
CC APPLICATION NUMBER: U.S. Serial No. 5712385 07/550,837
CC FILING DATE: 7/10/90
CC APPLICATION NUMBER: U.S. Serial No. 5712385 07/379,501
CC FILING DATE: 7/11/89
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Kaitburg, Richard J.
CC REGISTRATION NUMBER: 32,327
CC REFERENCE/DOCKET NUMBER: 196/189
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (213) 489-1600
CC TELEFAX: (213) 955-0440
CC TELEX: 67-3510
CC INFORMATION FOR SEQ ID NO: 12:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 28
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC SEQUENCE 28 BP: 6 A; 5 C; 10 G; 7 T; 0 OTHER.
SQ
Query Match 46.2% Score 12; DB 2; Length 28;
Best Local Similarity 77.3% Pred. No. 1.93e+02;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Db 5 CTGCTTAATTCAGTGGCTGAG 26
Cp 24 CTGCTTAATTCAGTGGCTGAG 3
RESULT 15
ID US-08-136-119-5 STANDARD; DNA; UNC; 34 BP.
AC xxxxxx
DE Sequence 9, Application US/08136119
CC Sequence 9, Application US/08136119
CC Patent No. 5473356
CC GENERAL INFORMATION:
CC APPLICANT: Helmbrook, David C.
CC APPLICANT: Hoyte, Mona I.
CC TITLE OF INVENTION: E-2F-2, A NOVEL MAMMALIAN TRANSCRIPTION
CC TITLE OF INVENTION: FACTOR
CC NUMBER OF SEQUENCES: 29
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: David A. Muthard
CC STREET: P.O. Box 2000, 126 Lincoln Avenue
CC CITY: Rahway
CC STATE: N.J.
CC COUNTRY: USA
CC ZIP: 07063-0907
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible

CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/136,119
CC FILING DATE:
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Multhard, David A.
CC REGISTRATION NUMBER: 35,297
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (908)594-3903
CC TELEFAX: (908)594-4720
CC INFORMATION FOR SEQ ID NO: 9:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 34 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: cDNA
CC SEQUENCE 34 BP; 6 A; 7 C; 11 G; 10 T; 0 OTHER.
S0

Query Match 46.2%; Score 12; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.93e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 12 CAGCCACTGGAT 23
|||||
Qy 5 CAGCCACTGGAT 16

RESULT 16
ID US-08-343-682-12 STANDARD; DNA; UNC; 35 BP.
AC xxxxxx
DT
DE Sequence 12, Application US/08343682
CC Sequence 12, Application US/08343682
CC Patent No. 5688511
CC GENERAL INFORMATION:
CC APPLICANT: Gaynor, Richard B.
CC APPLICANT: Ou, S.-H. I.
CC TITLE OF INVENTION: Cellular Protein TDP-43 and Regulation
CC TITLE OF INVENTION: of HIV-1 Gene Expression
CC NUMBER OF SEQUENCES: 17
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Arnold, White & Durkee
CC STREET: P.O. Box 4433
CC CITY: Houston
CC STATE: TX
CC COUNTRY: US
CC ZIP: 77210
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/343,682
CC FILING DATE: 22-Nov-1994
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Mayfield, Denise L.
CC REGISTRATION NUMBER: 33,732
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 713/787-1400
CC TELEFAX: 713/789-2679
CC TELEX: N/A
CC INFORMATION FOR SEQ ID NO: 12:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 35 base pairs
CC TYPE: nucleic acid

CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: DNA (genomic)
CC SEQUENCE 35 BP; 7 A; 9 G; 10 T; 0 OTHER.
S0

Query Match 46.2%; Score 12; DB 2; Length 35;
Best Local Similarity 77.3%; Pred. No. 1.93e+02;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Db 7 CTCAGATCGCATATAAGCAG 28
|||||
Qy 3 CTCAGATCGCATTTTAAAGCAG 24

RESULT 17
ID US-07-794-400-23 STANDARD; DNA; UNC; 36 BP.
AC xxxxxx
DT
DE Sequence 23, Application US/07794400
CC Sequence 23, Application US/07794400
CC Patent No. 5422104
CC GENERAL INFORMATION:
CC APPLICANT: Fiers, W.
CC APPLICANT: Tavernier, J.
CC APPLICANT: Van Ostade, X.
CC TITLE OF INVENTION: INF-Mutins
CC NUMBER OF SEQUENCES: 24
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Hoffmann-La Roche Inc.
CC STREET: 340 Kingsland Street
CC CITY: Nutley
CC STATE: New Jersey
CC COUNTRY: USA
CC ZIP: 07110
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/07/794,400
CC FILING DATE: 1991.11.20
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: EP 90810901.0
CC FILING DATE: 21-Nov-1990
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Krovatin, William
CC REGISTRATION NUMBER: 33256
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (201) 235-4387
CC TELEFAX: (201) 235-3500
CC INFORMATION FOR SEQ ID NO: 23:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 36 base pairs
CC TYPE: NUCLEIC ACID
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: DNA (oligonucleotide)
CC FEATURE:
CC NAME/KEY: misc_feature
CC LOCATION: 1..36
CC OTHER INFORMATION: /function= "PCR primer for
CC OTHER INFORMATION: mutagenesis"
CC OTHER INFORMATION: /note= "PCR primer for mutagenesis which is
CC OTHER INFORMATION: complementary to positions 219-184 of Seq. ID No. 54221
CC OTHER INFORMATION: 2 with mismatched bases at positions 7-9 and 11-12
S0

Query Match 46.2%; Score 12; DB 1; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.93e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Db 15 TCAGCCACTGGA 26
      |||||||
Cc 4 TCAGCCACTGGA 15

RESULT 18
ID US-08-041-648-13 STANDARD; DNA; UNC; 36 BP.
AC xxxxxx
DE Sequence 13, Application US/08041648
Cc Sequence 13, Application US/08041648
Cc Patent No. 5486463
Cc GENERAL INFORMATION:
Cc APPLICANT: Lesslauer, Werner
Cc APPLICANT: L. tscher, Hansruedi
Cc APPLICANT: St ber, Dietrich
Cc TITLE OF INVENTION: TNF-MUTAINS
Cc NUMBER OF SEQUENCES: 17
Cc CORRESPONDENCE ADDRESS:
Cc ADDRESSEE: George M. Gould, Esq., Hoffmann-La Roche Inc.
Cc STREET: 340 Kingsland Street
Cc CITY: Nutley
Cc STATE: New Jersey
Cc COUNTRY: U.S.A.
Cc ZIP: 07110-1199
Cc COMPUTER READABLE FORM:
Cc MEDIUM TYPE: Floppy disk
Cc COMPUTER: IBM PC compatible
Cc OPERATING SYSTEM: PC-DOS/MS-DOS
Cc SOFTWARE: Patent Release #1.0, Version #1.25
Cc CURRENT APPLICATION DATA:
Cc APPLICATION NUMBER: US/08/041,648
Cc FILING DATE: 1-APR-1993
Cc CLASSIFICATION: 435
Cc PRIOR APPLICATION DATA:
Cc APPLICATION NUMBER: EP 92810249.0
Cc FILING DATE: 2-APR-1992
Cc ATTORNEY/AGENT INFORMATION:
Cc NAME: Roseman, Catherine R.
Cc REGISTRATION NUMBER: 34240
Cc REFERENCE/DOCKET NUMBER: RAN 4105/147
Cc TELECOMMUNICATION INFORMATION:
Cc TELEPHONE: (201) 235-6208
Cc TELEFAX: (201) 235-3500
Cc INFORMATION FOR SEQ ID NO: 13:
Cc SEQUENCE CHARACTERISTICS:
Cc LENGTH: 36 base pairs
Cc TYPE: nucleic acid
Cc STRANDEDNESS: single
Cc TOPOLOGY: linear
Cc MOLECULE TYPE: DNA (genomic)
Cc HYPOTHETICAL: NO
Cc ANTI-SENSE: NO
Cc ORIGINAL SOURCE:
Cc ORGANISM: Primer 21/M6
Cc SEQUENCE 36 BP; 5 A; 11 C; 10 G; 10 T; 0 OTHER.

Query Match 46.2%; Score 12; DB 1; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.93e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0;

Db 15 TCAGCCACTGGA 26
      |||||||
Cc 4 TCAGCCACTGGA 15

RESULT 19
ID US-08-041-648-12 STANDARD; DNA; UNC; 36 BP.
AC xxxxxx
DE Sequence 12, Application US/08041648
Cc Sequence 12, Application US/08041648
Cc Sequence 12, Application US/08041648

Patent No. 5486463
GENERAL INFORMATION:
APPLICANT: Lesslauer, Werner
APPLICANT: L. tscher, Hansruedi
APPLICANT: St ber, Dietrich
TITLE OF INVENTION: TNF-MUTAINS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: George M. Gould, Esq., Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07110-1199
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/041,648
FILING DATE: 1-APR-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 92810249.0
FILING DATE: 2-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Roseman, Catherine R.
REGISTRATION NUMBER: 34240
REFERENCE/DOCKET NUMBER: RAN 4105/147
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-6208
TELEFAX: (201) 235-3500
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Primer 21/M5
SEQUENCE 36 BP; 4 A; 15 C; 9 G; 8 T; 0 OTHER.

Query Match 46.2%; Score 12; DB 1; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.93e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0;

Db 15 TCAGCCACTGGA 26
      |||||||
Cc 4 TCAGCCACTGGA 15

RESULT 20
ID US-08-397-470-22 STANDARD; DNA; UNC; 36 BP.
AC xxxxxx
DE Sequence 22, Application US/08397470
Cc Sequence 22, Application US/08397470
Cc Patent No. 5552353
Cc GENERAL INFORMATION:
Cc APPLICANT: Fiers, W.
Cc APPLICANT: Tavernier, J.
Cc APPLICANT: Van Oostede, X.
Cc TITLE OF INVENTION: TNF-Mutels
Cc NUMBER OF SEQUENCES: 24
Cc CORRESPONDENCE ADDRESS:
Cc ADDRESSEE: Hoffmann-La Roche Inc.
Cc STREET: 340 Kingsland Street
Cc CITY: Nutley
Cc STATE: New Jersey
```

CC COUNTRY: USA
CC ZIP: 07110
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/397,470
CC FILING DATE: 01-MAR-1995
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/794,400
CC FILING DATE: 20-NOV-1991
CC APPLICATION NUMBER: EP 90810901.0
CC FILING DATE: 21-NOV-1990
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Krovatin, William
CC REGISTRATION NUMBER: 33256
CC REFERENCE/DOCKET NUMBER: 4105/136-00
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (201) 235-4387
CC TELEFAX: (201) 235-3500
CC INFORMATION FOR SEQ ID NO: 22:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 36 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: DNA (oligonucleotide)
CC FEATURE:
CC NAME/KEY: misc.feature
CC LOCATION: 1..36
CC OTHER INFORMATION: /function="PCR primer"
CC OTHER INFORMATION: /note="PCR primer which is complementary to
CC OTHER INFORMATION: residues 219-184 of Seq. ID No. 5652353 2 with mismatched
CC OTHER INFORMATION: positions at positions 10-12."
CC
CC SEQUENCE 36 BP; 4 A; 15 C; 9 G; 8 T; 0 OTHER.
SQ
Query Match 46.2%; Score 12; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.93e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 15 TCAGCCACTGGA 26
|||||
4 TCAGCCACTGGA 15
OY
RESULT 21
ID US-08-397-470-23 STANDARD; DNA; UNC; 36 BP.
AC xxxxxx
DT Sequence 23, Application US/08397470
DE Sequence 23, Application US/08397470
CC Patent No. 5652353
CC GENERAL INFORMATION:
CC APPLICANT: Fliers, W.
CC APPLICANT: Tavernier, J.
CC APPLICANT: Van Ostade, X.
CC TITLE OF INVENTION: TNF-Mutlains
CC NUMBER OF SEQUENCES: 24
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Hoffmann-La Roche Inc.
CC STREET: 340 Kingsland Street
CC CITY: Nutley
CC STATE: New Jersey
CC COUNTRY: USA
CC ZIP: 07110
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/07/794,400
CC FILING DATE: 19911120
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:

CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/397,470
CC FILING DATE: 01-MAR-1995
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/794,400
CC FILING DATE: 20-NOV-1991
CC APPLICATION NUMBER: EP 90810901.0
CC FILING DATE: 21-NOV-1990
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Krovatin, William
CC REGISTRATION NUMBER: 33256
CC REFERENCE/DOCKET NUMBER: 4105/136-00
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (201) 235-4387
CC TELEFAX: (201) 235-3500
CC INFORMATION FOR SEQ ID NO: 23:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 36 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: DNA (oligonucleotide)
CC FEATURE:
CC NAME/KEY: misc.feature
CC LOCATION: 1..36
CC OTHER INFORMATION: /function="PCR primer for
CC OTHER INFORMATION: mutagenesis"
CC OTHER INFORMATION: /note="PCR primer for mutagenesis which is
CC OTHER INFORMATION: complementary to positions 219-184 of Seq. ID No. 56523
CC OTHER INFORMATION: 2 with mismatched bases at positions 7-9 and 11-12
CC
CC SEQUENCE 36 BP; 5 A; 11 C; 10 G; 10 T; 0 OTHER.
SQ
Query Match 46.2%; Score 12; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.93e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 15 TCAGCCACTGGA 26
|||||
4 TCAGCCACTGGA 15
OY
RESULT 22
ID US-07-794-400-22 STANDARD; DNA; UNC; 36 BP.
AC xxxxxx
DT Sequence 22, Application US/07794400
DE Sequence 22, Application US/07794400
CC Patent No. 5422104
CC GENERAL INFORMATION:
CC APPLICANT: Fliers, W.
CC APPLICANT: Tavernier, J.
CC APPLICANT: Van Ostade, X.
CC TITLE OF INVENTION: TNF-Mutlains
CC NUMBER OF SEQUENCES: 24
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Hoffmann-La Roche Inc.
CC STREET: 340 Kingsland Street
CC CITY: Nutley
CC STATE: New Jersey
CC COUNTRY: USA
CC ZIP: 07110
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/07/794,400
CC FILING DATE: 19911120
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:

```
CC APPLICATION NUMBER: EP 90810901.0.
CC FILING DATE: 21-NOV-1990
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Kroyatlin, William
CC REGISTRATION NUMBER: 33256
CC REFERENCE/DOCKET NUMBER: 4105/136-00
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (201) 235-4387
CC TELEFAX: (201) 235-3500
CC INFORMATION FOR SEQ ID NO: 22:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 36 base pairs
CC TYPE: NUCLEIC ACID
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: DNA (oligonucleotide)
CC FEATURE:
CC NAME/KEY: misc.feature
CC LOCATION: 1..36
CC OTHER INFORMATION: /function="PCR primer"
CC OTHER INFORMATION: /note="PCR primer which is complementary to
CC OTHER INFORMATION: positions 219-184 of Seq. ID No. 5422104.2 with mismatched
CC OTHER INFORMATION: residues at positions 10-12."
SQ SEQUENCE 36 BP; 4 A; 15 C; 9 G; 8 T; 0 OTHER.

Query Match 46.2%; Score 12; DB 1; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.93e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 15 TCAGCCACTGGA 26
OY 4 TCAGCCACTGGA 15
|||||

RESULT 23
ID 5256648-14 STANDARD; DNA; UNC; 42 BP.
AC xxxxxx
DE 01-JAN-1900
DE Patent No. 5256648.
CC APPLICANT: GASPARGO, FRANCIS P.; EDELSON, RICHARD L.
CC TITLE OF INVENTION: SELECTIVE INHIBITION OF GENE EXPRESSION
CC BY PHOTOACTIVATABLE OLIGONUCLEOTIDES
CC NUMBER OF SEQUENCES: 40
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/07/410,622
CC FILING DATE: 21-SEP-1989
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 299,265
CC FILING DATE: 23-JAN-1989
CC APPLICATION NUMBER: 146,571
CC FILING DATE: 21-JAN-1988
CC SEQ ID NO: 14:
CC LENGTH: 39
SQ Sequence 42 BP; 10 A; 10 C; 9 G; 10 T; 3 other;

Query Match 46.2%; Score 12; DB 5; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.93e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 25 CAGCCACTGGAT 36
OY 5 CAGCCACTGGAT 16
|||||

RESULT 24
ID 5256648-19 STANDARD; DNA; UNC; 42 BP.
AC xxxxxx
DE 01-JAN-1900
DE Patent No. 5256648.
CC APPLICANT: GASPARGO, FRANCIS P.; EDELSON, RICHARD L.

CC BY PHOTOACTIVATABLE OLIGONUCLEOTIDES
CC NUMBER OF SEQUENCES: 40
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/07/410,622
CC FILING DATE: 21-SEP-1989
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 299,265
CC FILING DATE: 23-JAN-1989
CC APPLICATION NUMBER: 146,571
CC FILING DATE: 21-JAN-1988
CC SEQ ID NO: 13:
CC LENGTH: 39
SQ Sequence 42 BP; 11 A; 10 C; 7 G; 11 T; 3 other;

Query Match 46.2%; Score 12; DB 5; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.93e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 8 CAGCCACTGGAT 19
OY 5 CAGCCACTGGAT 16
|||||

RESULT 25
ID 5256648-13 STANDARD; DNA; UNC; 42 BP.
AC xxxxxx
DE 01-JAN-1900
DE Patent No. 5256648.
CC APPLICANT: GASPARGO, FRANCIS P.; EDELSON, RICHARD L.
CC TITLE OF INVENTION: SELECTIVE INHIBITION OF GENE EXPRESSION
CC BY PHOTOACTIVATABLE OLIGONUCLEOTIDES
CC NUMBER OF SEQUENCES: 40
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/07/410,622
CC FILING DATE: 21-SEP-1989
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 299,265
CC FILING DATE: 23-JAN-1989
CC APPLICATION NUMBER: 146,571
CC FILING DATE: 21-JAN-1988
CC SEQ ID NO: 19:
CC LENGTH: 39
SQ Sequence 42 BP; 11 A; 10 C; 7 G; 11 T; 3 other;

Query Match 46.2%; Score 12; DB 5; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.93e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 8 CAGCCACTGGAT 19
OY 5 CAGCCACTGGAT 16
|||||

RESULT 26
ID 5256648-11 STANDARD; DNA; UNC; 49 BP.
AC xxxxxx
DE 01-JAN-1900
DE Patent No. 5256648.
CC APPLICANT: GASPARGO, FRANCIS P.; EDELSON, RICHARD L.
CC TITLE OF INVENTION: CELLULAR PROTEIN TDP-43 AND REGULATION
CC BY PHOTOACTIVATABLE OLIGONUCLEOTIDES
CC NUMBER OF SEQUENCES: 17
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Arnold, White & Durkee
CC STREET: P O Box 4433
CC CITY: Houston
```


SO SEQUENCE 50 BP; 9 A; 14 C; 13 G; 14 T; 0 OTHER.
Query Match 46.2%; Score 12; DB 4; Length 50;
Best Local Similarity 77.3%; Pred. No. 1.93e+02;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
DB 9 CTCAGATGCTGATATTAAGCAG 30
||||| ||||| ||||| ||||| |||||
QY 3 CTCAGCAGCTGATTTAAGCAG 24

RESULT 29
ID US-08-171-389-487 STANDARD; DNA; UNC; 50 BP.
AC xxxxxx
DE Sequence 487, Application US/08171389
CC Sequence 487, Application US/08171389
CC Patent No. 5726114
CC GENERAL INFORMATION:
CC APPLICANT: Edwards, Cynthia A.
CC APPLICANT: Cantor, Charles R.
CC APPLICANT: Andrews, Beth M.
CC APPLICANT: Turin, Lisa M.
CC APPLICANT: Fy, Kirk E.
CC TITLE OF INVENTION: Sequence-Directed DNA Binding
CC TITLE OF INVENTION: Molecules, Compositions and Methods
CC NUMBER OF SEQUENCES: 641
CC CORRESPONDENCE ADDRESS:
CC ADDRESS: Genelabs Technologies, Inc.
CC STREET: 505 Penobscot Drive
CC CITY: Redwood City
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 94063
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC OPERATING SYSTEM: IBM PC compatible
CC SOFTWARE: Patent Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/171.389
CC FILING DATE:
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/123,936
CC FILING DATE: 17-SEP-1993
CC PRIOR APPLICATION NUMBER:
CC APPLICATION DATA:
CC FILING DATE: 23-DEC-1992
CC PRIOR APPLICATION NUMBER: US 07/996,783
CC APPLICATION DATA:
CC FILING DATE: 27-JUN-1991
CC PRIOR APPLICATION NUMBER: US 08/081,070
CC APPLICATION DATA:
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Fabian, Gary R.
CC REGISTRATION NUMBER: 33,875
CC REFERENCE/DOCKET NUMBER: 4600-0175/G19P3
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 324-0880
CC TELEFAX: (415) 324-0960
CC INFORMATION FOR SEQ ID NO: 487:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 50 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: RNA (genomic)
CC HYPOTHETICAL: NO
CC ORIGINAL SOURCE:
CC INDIVIDUAL ISOLATE: Aids-associated retrovirus
CC INDIVIDUAL ISOLATE: (arv-2;proviral)
CC INDIVIDUAL ISOLATE: (arv-2;proviral)

SO SEQUENCE 50 BP; 8 A; 13 C; 13 G; 16 T; 0 OTHER.
Query Match 46.2%; Score 12; DB 1; Length 50;
Best Local Similarity 77.3%; Pred. No. 1.93e+02;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
DB 9 CTCAGATGCTGATATTAAGCAG 30
||||| ||||| ||||| ||||| |||||
QY 3 CTCAGCAGCTGATTTAAGCAG 24

RESULT 30
ID US-08-123-936-487 STANDARD; DNA; UNC; 50 BP.
AC xxxxxx
DE Sequence 487, Application US/08123936
CC Sequence 487, Application US/08123936
CC Patent No. 5726114
CC GENERAL INFORMATION:
CC APPLICANT: Edwards, Cynthia A.
CC APPLICANT: Cantor, Charles R.
CC APPLICANT: Andrews, Beth M.
CC APPLICANT: Turin, Lisa M.
CC APPLICANT: Fy, Kirk E.
CC TITLE OF INVENTION: Screening Assay for the Detection of
CC TITLE OF INVENTION: DNA-Binding Molecules
CC NUMBER OF SEQUENCES: 640
CC CORRESPONDENCE ADDRESS:
CC ADDRESS: Genelabs Technologies, Inc.
CC STREET: 505 Penobscot Drive
CC CITY: Redwood City
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 94063
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC OPERATING SYSTEM: IBM PC compatible
CC SOFTWARE: Patent Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/123,936
CC FILING DATE:
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/996,783
CC FILING DATE: 23-DEC-1992
CC PRIOR APPLICATION NUMBER:
CC APPLICATION DATA:
CC FILING DATE: 27-JUN-1991
CC PRIOR APPLICATION NUMBER: US 07/723,618
CC APPLICATION DATA:
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Fabian, Gary R.
CC REGISTRATION NUMBER: 33,875
CC REFERENCE/DOCKET NUMBER: 4600-0075.32/G19P2
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 324-0880
CC TELEFAX: (415) 324-0960
CC INFORMATION FOR SEQ ID NO: 487:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 53 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: RNA (genomic)
CC HYPOTHETICAL: NO
CC ORIGINAL SOURCE:
CC INDIVIDUAL ISOLATE: Aids-associated retrovirus
CC INDIVIDUAL ISOLATE: (arv-2;proviral)
CC INDIVIDUAL ISOLATE: (arv-2;proviral)
DB 9 CTCAGATGCTGATATTAAGCAG 30

Mon Aug 2 13:59:02 1999

US-09-121-239-27.ini

Page 14

|||||
QY 3 CTCAGCCACTGGATTTCAGCAG 24

Search completed: Mon Aug 2 12:23:25 1999
Job time : 84 secs.